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5.1.3
Compugen Ltd.
GenCore version
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protein search, using sw model OM protein - March 10, 2003, 12:15:04 ; Search time 10.2637 Seconds
 (without alignments)
327.825 Million cell updates/sec Run on:

US-09-816-989A-1

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

SCORE 80 84 70 5 71 72 70 70 60 70 60 70 60 70 60 8 60 8	+[::00		ر عو			SUMMAKIES	
84 50.6 384 2 843592 outer membrane 80.5 48.5 461 2 T03561 protein Part 64.6 372 2 G64064 outer membrane 74 44.6 372 2 G64064 outer membrane 74 44.6 372 2 G64064 outer membrane 72 43.1 210 2 A2550 histone H1 - se 70.5 42.5 206 2 S09388 histone H1 - se 70 42.2 206 2 S09388 probable NLP/P6 70 42.2 207 2 T34625 probable NLP/P6 70 42.2 1130 2 T34625 probable NLP/P6 70 40.4 394 2 G8576 probable NLP/P6 70 40.4 394 2 G8576 probable NLP/P6 70 40.1 1052 1 A44937 probable NLP/P6 86.5 39.8 1390 2 S51364 probable NLP/P6 86.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 86.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 86.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 86.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 96.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 PROBABLE NLP/P6 96.5 39.5 1528 2 A60338 probable NLP/P6 PROBABLE NLP/P6 96.5 39.5 1528 3 A60338 probable NLP/P6 96.5	No.	Score	Query	Length	DB	OI D	Description
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	53	63	38.0		7	JN0747	H

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•	H96835	T49622	T09127	S61926	T06257	AD1683	HSTRIR	840436	T10644	AG0592	T39683	T08942	AD1311	A82298	B87553	829309
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	63	63	63	62.5	62.5	62.5	62	62	62	62	62	62	62	62	62	61.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Cipacession: B43592
Rivelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, L.; Schoul Infect. Immun. 59, 3685-3693, 1991
A; Fitte: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum Transference number: A43592; MUID:91372983; PMID:1894368
A; Rocession: B43592
A; Accession: B43592
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A; Corosa-references: T-384 ex YEL-
A; Residues: T-384 ex YEL-
A; Corosa-references: GB:188563; NID:9155066; PIDN:AAA27480.1; PID:9155067
A; Cross-references: GB:188563; NID:9155066; PIDN:AAA27480.1; PID:9155067
A; Note: the authors translated the codon TIC for residue 316 as Tyr, and CGA for residue C; Keywords: membrane protein
                                                                                                                                                 C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
                                              outer membrane protein TmpB - Treponema phagedenis
                                                                                                  C; Species: Treponema phagedenis
B43592
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Query Match 50.6%; Score 84; DB 2; Length 384; Best Local Similarity 64.9%; Pred. No. 0.094; Matches 24; Conservative 5; Mismatches 6; Indels

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Gaps 7

1 AKKYAKKEKAAK-KAYKKEAKAKAA-EAAAKEAAYEA 35 ద ò

RESULT 2

hypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999
C;Accession: T03561
R;Vlcck, C; Pacces, V; Maltsev, N; Pacces, J; Haselkorn, R; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A,Residues: 1-461 <VLC>
A,Cross-references: BMBL:AF010496; NID:g3128256; PIDN:AAC16214.1; PID:g3128362
C,Genetics:
A,Map position: 1

Gaps 1; Length 461; Indels 8; 2; DB Score 80.5; DB Pred. No. 0.25; 5; Mismatches 48.5%; Query Match 48.5 Best Local Similarity 60.0 Matches 21, Conservative

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C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550; MUID:87040778; PMID:3022245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clacesion: A28100
R.Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A.Title: Characterization of the geneencocatence and transcriptional patterns of the geneencocatence number: A28100
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A.Residues: 1-211 < LAI > A.Residues: 1-211 < LAI > A.Residues: Caracterization of the geneencocatence in the cocatence of the geneencocatence of the geneencocatence
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N'Alternate names: protein B24P7.270
C'Species: Neurospora crassa
C'Species: Neurospora crassa
C'Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C'Accession: T50972
R'Schulte, U', Aign, V', Hoheisel, J', Brandt, P', Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Species: Strongylocentrotus purpuratus (purple urchin)
C,Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-210 «XNO»
A,Gross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C,Superfamily: histone HI
C,Superfamily: histone HI
C,Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-445 <SCH>
A;Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.270
A;Experimental source: BAC clone B24P7; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
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66.7%; Pred. No. 1.2;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.4%; Score 72; DB 59.0%; Pred. No. 1; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 23; Conservative
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nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: T50972
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A28100
histone H1-beta,
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Matches
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GG4064
Outcombrane integrity protein.tolA - Haemophilus influenzae (strain Rd KW20)
C.Species: Haemophilus influenzae
C.Date: 18-Aug-1955 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C.Accession: G64064, JG5212
C.Accession: G64064, JG5212
C.Accession: G64064, JG5212
C.Accession: JD.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, P.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, P.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Ritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64064
A;Residues: 1-372 criGR>
A;Accession: G64064
A;Residues: 1-372 criGR>
A;Cross-references: GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; TR:Sen, R; Ssikkema, D.J.; Murphy, T.F.
Gene 178, 75-81, 1996
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA a, beforence number.
                                                                                    C;Species: Peeudomonas aeruginosa
C;Species: Peeudomonas aeruginosa
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
S; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Journe 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83525
A;Accession: E83525
A;Accession: L347 <STO>
A;Residues: L347 <STO>
A;Resid
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A;Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-
A;Cross-references: GB:U32470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;TITLE: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA A;Reference number: JC5212; MUID:97080550; PMID:8921895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                    Fold protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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A;Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 76; DB 2; Length 347; ilarity 56.1%; Pred. No. 0.59; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.6%; Score 74; DB 2; Length 372; 58.1%; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAK---KEKAAKKAYKK---EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: strain PAO1
C, Genetics:
A, Gene: tolA; PA0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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les 18; Conserv
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A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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Best Local S:
Matches 23
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Best Loca Matches

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Gaps

10;

Indels

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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: JV0057; B4810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tola and tolB genes and localization of their produc
A;Reference number: JV0057; MUD: 90078104; PMID: 2687247
A;References number: JV0057; MUD: 90078104; PMID: 2687247
A;References: BIMAB 2222; NID: 9148018; PIDN: AA24683.1; PID: 9148019
A;Experimental source: strain JM105
A;Fille: The complete genome sequence of Escherichia coli K-12.
A;Fille: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID: 97426617; PM1D: 9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 11/2; 118/1; 156/2; 239/2; 308/2; 398/1; 458/3; 591/1; 640/3; 756/2; 790/2; 8
                       A; Accession: JC6552
A; Molecule type: mRNA
A; Molecule type: mlaryotic type I DNA topoisomerase
C; Genetics: dopl
C; Superfamily: eukaryotic type I DNA topoisomerase
C; Keywords: isomerase
F; 974/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C02F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 2; Length 1130;
Pred. No. 6.4;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                              Length 1015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: U41545; PIDN: AAA83190.1; CESP: C02F12.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 KKEVKKEDTAKKDVKKEVKKETPKKTPAKRKAAESSSEESDF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R'Miller, N. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid CO2F12. A; Reference number: 221473
A; Reference number: JC6552; MUID: 98245940; PMID: 9583949
                                                                                                                                                                                                                                                                                                                                                                                                                           ----- AKAKAAEAAKEAAY 33
                                                                                                                                                                                                                                                                                                                                                                      .
8
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Pred. No. 5.9;
6; Mismatches 8
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.4%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKYAKKEKAAKKAYKKE-
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A; Residues: 1-1130 <MIL>
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DNA topoisomerase (BC 5.99.1.2) - slime mold (Physarum polycephalum)
NALternate names: emega-protein; micking-closing enzyme; type I DNA topoisomerase
C;Species: Physarum polycephalum
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: UC6552
R;Czerwinski, R.M.; Lipniacki, A.; Staron, K.
Gene 209, 39-44, 1998
A;Title: cDNA cloning of Physarum polycephalum DNA topoisomerase I and expression analys
                                                                                                                                                                                                                                                                       RESULT 8

903188
histone H1 - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S03388
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chrom A;Reference number: S09388; MUID:90060019; PMID:2583125
A;Accession: S09388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL078618; PIDN:CAB44532.1; GSPDB:GN00070; SCOEDB:SC10A7.22 A;Experimental source: strain A3(2) C;Genetics:
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0
                       Length 445;
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Pred. No. 1.6;
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                                                                               Indels
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                       Score 70.5; DB 2;
Pred. No. 2.7;
4; Mismatches 10;
                                                                                                                                                                        93 AAKOAKIDLAEAKKKAAEAKKKAEEAARKEAAERA 127
                                                                                                                                     2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
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42.2%; Score 70; DB:
Best Local Similarity 54.3%; Pred. No. 2.1;
Matches 19; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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56.7%;
                       42.5%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-206 <HTL>
C;Superfamily: histone HI
C;Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: SCOEDB:SC10A7.22
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922 ASKTAPKKAAAKPAAKKAAPKKAASKSAKTPAAKA 956
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me : 12.2637 secs
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues:1-394 <STO>
A;Residues:1-394 <STO>
A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C)Species: Escherichia coli (5. Species: Escherichia coli (5. Species: Apodaca, A) Fitte: Genome sequence of enterchemorrhagic Escherichia coli (157:H7.
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0774
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                                                                                                                                                                                                                                                                                         Length 421;
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Pred. No. 5.6;
5; Mismatches 8; Indels
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48.9%; Pred. No. 5.6;
iive 5; Mismatches 8; Indels
                                                                                                                                                              C.Keywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;78-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                    Score 69.5; DB 2;
Pred. No. 3.2;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                40.4%;
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Best Local Similarity 52.6%;
Matches 20; Conservative
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Matches 22, Conservative
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Best Local Similarity 48.9
Matches 22, Conservative
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A; Status: preliminary
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DNA topoisomerase I - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accesion: G78403
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mal S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Resdiques: 1-1021 «WHI»
A).Cross-references: GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF10943.1; PID:g645912'
A;Experimental source: strain R1
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40.4%; Score 67; DB 2; Length 1021;
Best Local Similarity 51.4%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 14; Indels
                                                                         167 AKKKAEAEAAKAAAEAQKKAEAAAALKKKAEAAEAAAAEAKKA 211
32
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C,Superfamily: bacterial type I DNA topoisomerase
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 7.97468 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

US-09-816-989A-1 166 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P29720 treeponema p P50600 pseudomonas P44678 haemophilus P06144 lytechinus P06144 lytechinus P06144 lytechinus P06144 lytechinus P19934 escherichia P19934 escherichia P40269 trypanosoma P40269 trypanosoma P40268 trypanosoma P95109 mycobacteri P51979 streeptococc P19979 streeptococc P1
SUMMARIES	TWPB TREPH TOLA_PSEAE TRYCR ASR_BYTCL HIG_STRPU SPAA_STRDO HIG_STRPU SPAA_STRDO HIG_STRPU SPAA_STRDO HIG_STRPU SPAA_STRDO HIG_TRYCR HIG_STRPU NOCHA HIL_VOLCA TRYCR HIL_VOLCA TRYCR HIL_VOLCA TRYCR HIL_PRAN HIL_VOLCA TRYCR HIL_PRAN HIL_VOLCA TRYCR HIL_PRAN HIL_VOLCA TRYCR HIL_VOLCA TRYCR HIL_VOLCA HIL_CHITE HIL_VOLCA HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE HIL_CHITE
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Length	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
* Query Match	7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Score	744 744 744 744 744 744 744 744 744 744
Result No.	33333355555555555555555555555555555555

Q53956 streptomyce Q9zf22 proteus vul Q9x909 streptomyce Q8yj59 brucella me Q05831 mytilus tro P50887 drosophila Q22918 caenorhabdi P28350 neurospora Q9rq15 bacteroides Q14093 homo sapien P10922 mus musculu P43278 rattus norv
SECF STRCO IF2_FROVU TOP1_STRCO RS16_BRUME H1L_MYTTR R12_DROME IF5_CABEL SYV_NEUCR SYV_NEUCR CYL2_HUMAN H10_MOUSE
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373 9173 952 134 200 200 200 100 100 1103 1103
337.0 337.0 336.7 7.7 7.7 7.7 7.7 7.7 7.7 7.7 7.7 7.7
61.5 61.5 61.5 61.6 61 61 60.5 60.5 60.5
8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

TREPH TYPE TREPH TYPE TREPH TYPE TREPH TYPE TREPH TYPE TREPH 51-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 101-APR-1993 (Rel. 26, Last sequence update) TYPE 1993 (Rel. 26, Last sequence update) TYPE 1993 (Rel. 26, Last sequence update) TYPE TREPONEMENT TREPH TYPE TREP	SEQUENCE FROM N.A. STEAIN=Kazan 5; MEDLINES91372881; bubmed=1894368; MEDLINES91372881; bubmed=1894368; MEDLINES91372881; bubmed=1894368; MEDLINES91372881; bubmed=1894368; Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991."; I- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR LARGE MOLECULAR LOCATION: OUTER MENBRANE-ASSOCIATED. I- SUBCELLULAR LOCATION: OUTER MENBRANE-ASSOCIATED. I- SIMILARITY: TO TMPB OF T.PALLIDUM. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-ch).	MEMBRANE PROTEIN B. ANDEM REPEATS OF K-A-A-[AKR]-
TREPH STANDARD; (0) -R-1993 (Rel. 25, Create -R-2001 (Rel. 45, Last - 5, Last - 6, Last - 6, Last - 6, Last - 7, Last - 7, Last - 8, Last - 8, Last - 1, Las	SEQUENCE FROM N.A. STRAIN=Kazan 5; STRAIN=Kazan 5; STRAIN=Has=913729813; pubMed=1894368; Weblion D.B., Limberger R.J., Curci K., M Sliviensky L., Schouls L.M., van Embden "Treponema phagedenis encodes and expres pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991)!- FUNCTION: TMP MAY SERVE AS A PORIN O LARGE MOLECULES!- SUBCELLULAR LOCATION: OUTER MEMBRANE -!- SUBCELLULAR LOCATION: OUTER MEMBRANE -!- SIMILARITY: TO TMPB OF T.PALLIDUM. This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfor the Buropean Bioinformatics Institutions as lon modified and this statement is not removentiles requires a license agreement (S	EMBL, MS8863; AAA27480.1; PIR, B43892; B43892. Antigen; Outer membrane; Rep SIGNAL 22 384 CHAIN 22 384 COMAIN 151 235 CHAIN 151 155 REPEAT 166 170 REPEAT 166 170 REPEAT 166 170 REPEAT 166 170 REPEAT 167 180 REPEAT 167 180 REPEAT 171 195 REPEAT 191 195 REPEAT 191 195 REPEAT 196 200 REPEAT 201 205 REPEAT 201 205 REPEAT 201 205 REPEAT 201 205 REPEAT 216 220
SUL		<b>BP4000 KKKKKKKKKKKK</b>
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Transport; Protein transport; Transmembrane; Repeat; Inner membrane;

EMBL; AE004530; AAG04360.1;

Complete proteome.

POTENTIAL. PERIPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL)

16 37 347 216

TRANSMEM

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STRAIN=ATCC 15692 / PAO1;

MEDLINE=204331317; PubMed=10984043;

MEDLINE=20431317; PubMed=10984043;

Stover C.K., Pham. F.L., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., For B., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
     1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
A-A-E.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
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                                                                                                                                                                                                                                                                                                                          Length 384;
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                                                                                                                                       Score 84; DB 1;
Pred. No. 0.059;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA
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5; Mismatches
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22-3.
5-4.
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J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                      42677 MW;
                                                                                                                                                                                                                                                                                                                          50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO N-TERMINUS
                                                                                                          243
252
261
270
279
288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                   245
254
263
272
281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tola protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOLA PSEAE P50600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIR=Rd / KW20 / ATCC 51907;

STRAIR=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Pritchman J.L., Euhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !ransport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                           Score 76; DB 1; Length 347; Pred. No. 0.35;
                                                                                                                                                                                              7; Indels
                                                                                                                        347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                     1 AKKYAK---KEKAAKKAYKK---EAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                   TOLAH HABIN STANDARD; PRT; 372 AA. P44678; P94810; 01-NOV-1995 (Rel. 32, Created) 15-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                              5; Mismatches
                                                                                                                                                             45.8%;
56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32722; AAC22041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995)
                                                                                                                                                                                                Conservative
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P19934; 1TOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tola protein.
TOLA OR HI0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGR; HI0383;
                                                                                                                                                                Local Sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1479
                                                                                                                                                         Query Match
                                                                                                                        SEQUENCE
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Local Similarity
ses 23; Conserv
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H1B_STRPU
ID_H1B_STRPU
AC_P15869;
                                                                                                                      DBH MYCSM
Q9ZHC5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
  Query Match
             Best Loc
Matches
                                                                                                RESULT 5
DBH MYCSM
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                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                               Lytechinus pictus (Painted sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Nuclear protein; DNA-binding; Multigene family.
210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:812-8133(1986).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAIN INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                          AKAAAEAKAKA (IN STRAIN 1479).
A (IN STRAIN 1479).
F (IN STRAIN 1479).
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knowles J.A., Childs G.J., "Comparison of the sea urchins
                                                                                                                                                                                                         44.6%; Score 74; DB 1; Length 372;
                                                                                                                                                                                                                                 8; Indels
                                                               > P (IN STRAIN 1479).

> R (IN STRAIN 1479).

> A (IN STRAIN 1479).

> A (IN STRAIN 1479).
                                                                                                                                                                                      266ECF05C6C95544 CRC64;
                                                                                                                                         I -> V (IN STRAIN 1479).
N -> S (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
S -> P (IN STRAIN 1479).
                                           -> A (IN STRAIN 1479).
           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Late histone H1.
                                                                                                                                                                                                                       0.58;
                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                  5 AKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001386; Histone H1/H5.
InterPro; IPR003116; Linkerhist N.
Pfam, PP00538; linker histone; I.
BroDom; PD000373; Linkerhist N; I.
SMART; SM09526; H15; I.
                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDLINE=87040778; PubMed=3022245;
                                                                                                                                                                                      39831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X04488; CAA28177.1; -. PIR; A25550; A25550.
                                                                                                                                                                                                                      58.1%;
                                                                                                                                                                                                                                18; Conservative
                                                     142
1165
2237
2332
234
254
306
326
326
326
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                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
 Complete proteome DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ytechinus.
                                                                                                                                                                                                                                                                                                                                H1 LYTPI
P06144;
                                                                                                                                                                         VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                     PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Gen. Genet. 260:475-479 (1998).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKRAYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DRATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee B.H., Murugasu-Oei B., Dick T.; "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.
DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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21230 MW; CASF577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11,
                                                          6
                                                                                                                                                           157 AKKAAKKAAKKAAKKPAKKAAKKAAKPA 195
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                                                                                                                           1 AKKYAKK---EKAAKK-AYKKEAKAKAAEAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-beta, late embryonic.
43.4%; Score 72; DB 1, 59.0%; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAAKKAYKKEA-KAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                          208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00216; Bac DNA binding; 1.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; Pubmed=9894918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF068138; AAD13809.1; -.
HSSP, P02346; 1HUU.
InterPro; IPR000119; Bac_DNAbind.
                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium smegmatis.
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Gaps

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STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MSDLINE=97061202; PubMed=8905232;
Oshlma T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levengood S.K., Webster R.E., "Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rilety M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97133271; PubMed=8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levengood S.K., Beyer W.F. Jr., Webster R.E.; membrane protein involved in colicin uptake contains an extended helical region."; membrane protein involved in colicin uptake region."; Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                         Score 70; DB 1; Length 1130;
Pred. No. 3.7;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                   121 779 COILED COIL (POTENTIAL).
805 1061 COILED COIL (POTENTIAL).
1130 AA; 131485 MW; BOFDZEFE3D99FB09 CRC64;
                                                                                                                                                                                                                                                                                       1016 KREEASEKRTRKEAEKKAEKEKAEKAAKEAAKE 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    421 AA
                                                                                                                                                                                                                                                               6 KKEKAAKKAYKKEAKAKA-----AEAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tola protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
                        EMBL, U41545; AAK39135.1; -. Wormbep; C02F12.7; CE03901. Hypothetical protein; Colled coil. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90078104; PubMed=2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91296736; PubMed=2068069;
                                                                                                                                                                                               ilarity 51.4%;
Conservative
                                                                                                                                                                             42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH PORINS
                                                                                                                                                                                           Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                               TOLA ECOLI
P19934;
                                                                                                                                SEQUENCE
                                                                                                                                                                           Query Match
                                                                                                            DOMAIN
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    S목품활투투 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb.sib.ch).
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                  MEDLINE-88246461; PubMed=2837660;
Lai Z.-C., Childe G.;
"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
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                                                                                                                                                                                                                                      Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
--- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION (NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
---- SUBCELLULAR LOCATION: Nuclear.
--- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller N.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 131.5 kDa protein C02F12.7 in chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.1%; Score 71.5; DB 66.7%; Pred. No. 0.65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PP00538; linker histone; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: WEAK, TO MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M20314; AAA30052.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28100; A28100.
                                                               Strongylocentrotus.
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                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
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                                                                                     NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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g

Gaps

3;

us-09-816-989a-1.open.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                  Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 87 AA; 9005 MW; 843FF90F5F73922D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal protein, Nuclear protein, DNA-binding, Multigene family SEQUENCE 97 AA; 10290 WW; AA8073FDBA36121B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Thlahuen 2;
MEDLINE=95059220; PubMed=7969272;
Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,
Galanti N., Pettersson U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A gene family encoding heterogeneous histone H1 proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.3%; Score 68.5; DB 1; Length 97; 52.6%; Pred. No. 0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYA---KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
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01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      41.3%; Score 68.5; DB ilarity 52.6%; Pred. No. 0.62; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acid shock protein precursor.
                                                                                                                                                                                                                                                                       EMBL; L27120; AAA66479.1; -.
                                                                                                                                                                                                                                                                                                         EMBL; L27117; AAA66481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L27115; AAA66478.1; -.
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es 20; Conserv
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Matches
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H1C2_TRYCR
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ASR ENTCL
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecodene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                       Lubkowski J., Hennecke F., Plucckthun A., Wlodawer A.;
"Filamentous phage infection: crystal structure of g3p in complex
with its coreceptor, the C-terminal domain of TolA.";
Structure 7:711-722(1999).

-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A
COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE
COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Tulahuen 2;
MEDLINE=95059220; PubMed=7969272;
Asslund L., Carisson L., Henriksson J., Rydaaker M., Toro G.C.,
Galanti N., Pettersson U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n.
                  "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galanti N., Pettersson U., "A gene family encoding heterogeneous histone H1 proteins in Trypanosoma cruzi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.5; DB 1; Length 421; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Inner membrane; 3D-structure; Complete proteon DOMAIN 1 13 CYTOPLASMIC (POTENTIAL). TRANSMEM 14 34 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASMIC (POTENTIAL)
                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KYAKKEKAAKKA-----YKKEAKAKAABAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000177; AAC73833.1; -. EMBL; D90713; BAA55405.1; -. PIR; JV0057; JV0057. PDB; ITOL; 20-MAY-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M28232; AAA24683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND LAMB
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
HICG_TRYCR
AC P4026 JI
AC P4026 JI
DT 01-FEB-
DT 01-NOV-
DE Histon(
OC EUKARY,
OX NCBI_TI
RN [1]
RN SEQUEN(
RC STRAIN:
RX ABBLINI
RX A
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Gaps

3.

Gaps

6

us-09-816-989a-1.open.rsp

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                  InterPro, IPR001386; Histone H1/H5.
InterPro, IPR00316; Linkerhist. N.
Pram, PR00538; linker histone; J.
ProDom, PD000373; Linkerhist. N. 1.
SMART, SMO826; H15, 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Westendorf J.M.; "Identification of novel M phase phosphoproteins by expression
                                                                                                                                                                                                40.1%; Score 66.5; DB 1; Length 217; 50.0%; Pred. No. 2.1; tive 3; Mismatches 8; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97039687; PubMed=8885239;
Matsumoto-Taniura N., Pirollet F., Monroe R., Gerace L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32F269B4A532AD46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Zuotin related factor-1 (M-phase phosphoprotein 11)
ZRF1 OR DNAJC2 OR MPHOSPH11 OR MPP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AKKPAAKKPAAKKAKPAKKVAKPAKKAAAKPAKAAAKPA 201
                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAAKKAYK-----KEAKAKAAEAAKEA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperone, Nuclear protein, Phosphorylation.
DOMAIN 94 163 J-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.1%; Score 66.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 605502; ...
InterPro; IPR001623; DnaJ N.
InterPro; IPR001005; Myb DNA_binding.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00249; myb DNA-binding; 2.
SWART; SM00271; DnaJ; 1.
SWART; SM00395; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00037; MYB_1; PALSE_NEG.
PROSITE; PS500334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X98260; CAA66913.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biol. Cell 7:1455-1469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65913 MW;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:13192; ZRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 AA;
HSSP; P02259; 1HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxiD=9606;
                                                                                                                                                                                                       Ma.
Local br.
20;
                                                                                                                                                                                                                                                                                                                                                                                                                        ZRF1_HUMAN
ID ZRF1_HUMAN
                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099543;
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
SERBERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDIANE-87172742; Pubmed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; Knowles J.A., Lai Z.-C., Childs G.J.; "Isolation, characterization, and expression of the gene encoding the late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrorus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i - FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-i - SUBCELLULAR LOCATION: Nuclear.
-i - SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                  Seputiene V., Motiejunas D., Suziedelis K., Suziedeliene E., "Molecular characterization of acid-inducible Asr protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.3%; Score 68.5; DB 1; Length 101; 52.8%; Pred. No. 0.7; tive 5; Mismatches 7; Indels 9
                                                                                                                                                                                           Escherichia coli.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ASR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACID SHOCK PROTEIN.
0FAF9D6EED61D26E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAK----KEKAAKKAYKKEAKAKAAEAAAKEAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF405542; AAK92015.1; ALT INIT.
InterPro; IPR000104; Antifreeze_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 7:478-485(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 101 AC
101 AA; 10254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M16033; AAA30059.1; -. PIR; A26721; A26721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone H1-gamma, late.
                    Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                             SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=550;
                                                          Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purpuratus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIG STRPU
P07796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
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HIG_STRPU
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABELIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
  JNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa
                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634210;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamiin N., Holroyd Shornsby T., Jagels K., Krogh A., McLean U., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat; Complete proteome.
DOMAIN 1 90
BACTERIAL HISTONE-LIKE DOMAIN.
                       laminin-2-binding protein).
HUP OR HLP OR LBP21 OR RV2986C OR MT3064 OR MTCY349.01.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEGENERATE REPEATS REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1997) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 39.5%; Score 65.5; DE 1 Similarity 52.4%; Pred. No. 2.6; 22; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001386; Histone H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 71-86, AND DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00216; Bac_DNA_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00624; HĪSTONEHS.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
· 22187 MW; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE007127; AAK47393.1;
HSSP; P02346; 1HUU.
TIGR; MT3064; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z83018; CAB05427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculist; Rv2986c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Savita P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Petrygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.8%; Score 66; DB 1; Length 1391; 48.7%; Pred. No. 11; tive 1; Mismatches 9; Indels
                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKYAKK-----EKAAKKAYKKEAKAKAEAAKE 30
                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
10-FEB-1995 (Rel. 31, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Axoneme_associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656, ККІЛАККЕКЕТАЕКККСЕКААККККЕААЕКККСАЕЛАККЕ
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(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                      - 281 KKFKEEEKAKKEAEKKAKAEAKRKEQEAKEKQRQA 315
48.6%; Pred. No. 4.7; ive 7; Mismatches
                                                              2 KKYAKKEKAAKKAYKK-EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                             PRT; 1391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0020733; Dhyd\mst101(2)
                                                                                                                                                                                                                                                                                                                                MST101(2).
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X73481; CAA51876.1; -
                     17; Conservative
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                                                                                                                                                                                                         STANDARD;
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les 19; Conserv
Local Similarity
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15-JUL-1999
16-OCT-2001
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P95109;
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RESULT 14
MST2 DROHY
MST2 DROHY
ACC 0086 50 DI
DT 01-FEB

S.L.,

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Harris

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Gaps

7;

Indels

~ Matches

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DBH MYCTU ID DBH M AC P9510 DT 15-JU DT 15-JU

Search completed: March 10, 2003, 12:17:07 Job time : 8.97468 secs

us-09-816-989a-1.open.rspt

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Q9vwk3 drosophila
Q9xhe2 chlamydomon
Q9x342 bacillus an
Q9vfh1 drosophila
Q45302 corynebacte
Q9ant7 brevibacter
Q8uw1 encephalito
Q46142 mytilus edu
         Q9agv7 corynebacte
Q98fb4 rhizobium 1
Q9mf6 trypanosoma
Q8x965 escherichia
Q9vbl3 drosophila
Q9vpl0 deinococcus
                                                                Q9nfj8 trypanosoma
Q9nfj8 trypanosoma
Q9nfj4 trypanosoma
Q9nfj9 trypanosoma
Q9nfj9 trypanosoma
Q60415 homo sapien
G60414 homo sapien
G90419 plasmodium
Q2638 trypanosoma
Q902d7 bufo bufo g
Q39576 chlamydomon
Q903p19 arabidopsis
Q91p19 arabidopsis
Q81m3 ralstonia s
017321 chironomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MT-2;
MEDLINE=56198174; PubMed=8626299;
ROTIGUEZ-HETVA J.J., Ramos-Gonzalez M.I., Ramos J.;
ROTIGUEZ-HETVA J.J., Ramos-Gonzalez M.I., Ramos J.;
RTPH PSEUGOMODAS putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
"Characterization Oprl null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5835-5840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MT-2;
Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         372 AA.
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                                                                                             Q9N6L9
Q9NFJ9
O60414
Q9ND19
Q26939
Q305D7
Q39576
Q8VWK4
                           Q9NFP6
Q8X965
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Q9XHE2
Q9X342
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Q8XWI3
          Q9AGV7
Q98FB4
                                                        Q9RUL0
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Q45302
Q9ANT7
Q8SUW1
Q46142
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                                               O9VBL3
                                                                                      D9NFJ4
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Bacteriol. 178:1699-1706(1996)
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                  582
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969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                         Tola protein.
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09WWX1
068124 rhodobacter
Q8wq44 leishmania
Q8t5r3 leishmania
Q01395 drosophila
Q937K4 erwinia chr
Q9bmy8 leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95uns trypanosoma
Q9xz07 drosophila
Q95un6 trypanosoma
Q9xy5 leishmania
Q9kj98 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ajx2 streptomyce
Q9p3q8 neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094705 physarum po
095un5 trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29wwx1 pseudomonas
                                                              March 10, 2003, 12:15:01 ; Search time 18.5338 Seconds
    (without alignments)
    389.109 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                         1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                          671580 segs, 206047115 residues
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                                             protein search, using sw model
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066124
086124
080144
081395
0011395
098AX2
098AX2
098AX2
098AX0
094705
094705
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
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Maximum Match 100%
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sp_bacteria:*
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length: 2000000000
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sp_virus:*
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Match
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Minimum DB seq Maximum DB seq

Database

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Q9XYY5 Q9KJ98

75.5 70.5 70.5 70 69.5 68.5

80.5 79.5 77 77

Score

80.

Matches

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88 8 8 8 8 8 8 8

RESULT 2

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 X 16 AA APPROXIMATE TANDEM REPEATS OF X-{KQ]}-K-C-{AE}-E-X-A-[X]-K-X-X-X-X-
                                                                                                                                                                                                                                                                                                                             Papageorgiou F., Soteriadou K.;
"Identification of a Leishmania infantum gene encoding for an histone
                                                                                                                                                                                                                                     Leishmania infantum.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.9%; Score 79.5; DB 5; Length 111; 67.6%; Pred. No. 0.09; ive 3; Mismatches 5; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 5; Length 275;
Pred. No. 0.42;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                               HI-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF469106; AAL76335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- TISSUB SPECIFICITY: TESTIS (BY SIMILARITY).
-i- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AA; 11162 MW; 16168F3B54960E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
Axoneme-asciated protein MST101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 AKKKAAEEAAKKKAEEVAAKKKADEAAAKKKCAEA 230
                                                                                                                               111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 АККУАККРАККААККРАККРАК-КААККААККАА 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 AA
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   32
                                     95
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                                                                                                                                                                 Created)
                                                                                                                             PRT;
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57.1%;
                                                                                                                                              Q8T9R3;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.6
Matches 23; Conservative
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                                                                                                                                                                                                                        18 kDa nuclear protein.
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Local St.
20;
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NGI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tzortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K.P., "Identification and characterization of a novel Leishmania gene encoding for a putative histone Hi- like transcription factor."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ237814; CAD21431.1; -.
                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 49.5 kDa protein.
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                             . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE...
STRAIM-SEND03;
MEDLINE=97404404; PubMed=9256491;
MEDLINE=97404404; PubMed=9256491;
Vlcek C., Pacces V., Maltsev N., Pacces J., Haselkorn R., Fonstei Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S. A. 94:9384-9388(1997).
EMBL; AF010496; AAC16214.1;
Hypothetical protein.
SEQUENCE 461 AA; 49516 MW; DD8DA03418BC0368 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
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Pred. No. 0.08;
3; Mismatches 5; Indels
                                                                                        Length 372;
                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                    40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0A4AB93089D6C261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                    160 AKKKAEDEAKKKAEBEAKKAAAEBAKKKAAEDAKKKAAEBA 200
                                                                                                                                                                 1 AKKYA-----KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                        Match 48.8%; Score 81; DB 2; Local Similarity 56.1%; Pred. No. 0.21; les 23; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80.5; DB Pred. No. 0.29;
                                                                                                                                                                                                                                                                                             461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AKEVVEKEAAAKDAAAKEAKAR-EEAAAKDAAKA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
EMBL, X74218; CABS0780.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; HISTONEHS.
                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 67.6%;
Matches (23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08W044;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
n1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 AA; 9999 MW;
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                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 kDa nuclear protein.
                                                      372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein.
                                                    SEQUENCE
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             PERTAINAGE (2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DB 3; Length 445;
Pred. No. 3.6;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 16; Length 244; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Neurospora genome project;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389890, CAB97292.1; -.
HSSP, P25685, 1HDJ.
INTEPPC; IRRO1623; DNaJ.N.
PFam; PF00226; DNaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00076; DNaJ 1; UNKNOWN_1.
PROSITE; PS00076; DNaJ 2; 1.
SROGIES PS00076; DNAJ 2; 1.
SROUSNCE 445 AA; 50612 MW; 982B97EFAZDA34E6 CRC64;
                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 KKRLEKEAAEKKAAEEAAKKAAEEAAAKEAEEKA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AKKEAAAKKATAKKATAEKKAAAEKAAAKRAAKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AKKEKAAKKAYKKEA----KAKAAEAAKEAAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 45.2%;
Local Similarity 61.8%;
es 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
Streptomyces coelicolor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                     NCBI_TaxID=1902
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9P3Q8
Q9P3Q8;
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Q9XAQ3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI TaxID=5659;
                                                                                                                                                                                                                                                                                                               Erwinia chrysanthemi.
Bacteria; Proteobacteria; gamma subdívision; Enterobacteriaceae;
Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAY M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
"characterization of the Erwinia chrysanthemi tol-pal genes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAS2708.1; -.
SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melo G.S., Fragoso S.P., Fasel N.S., Mendonca S.C.F.; "Cloning and sequencing of histone H1 gene from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.4%; Score 77; DB 2; Length 395;
51.2%; Pred. No. 0.61;
tive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF287632; AAG66088.1; -.
Interpro; IPR001386; Histone H1/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 101 AA; 10078 MW; 3D3AE865FD9B6846 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AKKKAEEBAKAKAAADAKQKAEEBAKAKAAAAKEKAAADA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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45.5%; Score 75.5; DB 5;
Best Local Similarity 55.3%; Pred. No. 0.23;
Matches 21; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK---EKAAKKAYKKEAKAKAAEAAKEAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AA.
                                                                                                                395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AA
                                                                                                                                                                          Created)
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                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel: 19,
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative secreted protein. SCO1805 OR SCI33.04.
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Matches 21; Conservative
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                         TolA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=3937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                          Q937K4
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RESULT 7
298MY8
AC 098M
AC 098M
AC 098M
DT 01-J
DT 01-J
DT 01-J
DT 01-J
DT 01-J
DT 01-M
DE Hist
CS Euka
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OC Euka
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Gaps

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Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Berrydota; Metazoa; Brdopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porto R.M., Amino R., Elias M.C.Q., Faria M.B., Schenkman S.; "Histone H1 is phosphorylated in non-replicating and infective forms of Trypanosoma cruzl."; Submitted (Jul-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV046274; AAL02283.1; -. NON TER 78
                                              Score 70; DB 5; Length 1015;
Pred. No. 9.3;
6; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%; Score 69.5; DB 5; Length 78; 52.6%; Pred. No. 0.8; tive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          1015 AA; 112051 MW; FC6A756029C868F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AA; 8067 MW; 8417971A6FEF050B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKYAKKEKAAKKAYKKE------AKAKAAEAAKEAAY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 AKKRAAPKKKPAAKKAVNKSAKKHAAKKAPKKAVKKA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYA---KKEKAAKKAYKKEAKAKAAEAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.99
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 52.6
20; Conservative
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BCDNA: LD21177 OR CG8431.
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  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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1D 009
DD 001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=A3(2) / M45;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.P., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(202).

EMBL, AL078618; CAB44532.1; -.

ELMBL, PRO0877; NLPC P60.

Pfam; PP00877; NLPC P60.

SEQUENCE 277 AA; 27694 MW; C53669505187B256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            Saunders D.C., Harris D.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                 Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                           Putative NLP/P60 family secreted protein.
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                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                     SCO4561 OR SCD16A.22.
Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
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Gaps

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[1] SEQUENCE FROM N.A

094705

RESULT 11
024705
DD 0Q4700
AC 09470
DT 01-FE
DT 01-DE
DE DNA t
GN TOP1.
CS Physa
OC Bukar
OC Physa
OX (1)

Matches

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Last sequence update) Last annotation update)

Created)

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                                                                     PRELIMINARY;
                                                                                095UN6;
                                                                   095UN6
                                          RESULT 14
                                                       Q95UN6
ID Q9
AC Q9
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83 AA.

PRT;

Gaps

5;

6; Indels

4; Mismatches

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEA 31

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Trypanosoma cruzi.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                   Porto R.M., Amino R., Elias M.C.Q., Faria M.B., Schenkman S., "Histone Hl is phosphorylated in non-replicating and infective forms of Trypanosoma cruzi."; Lemb. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY046273; AALO2282.1; -- 83 83

SEQÜENCE 83 AA, 8592 MW, 7PAD924B1A6BD92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYA---KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.6
Matches 20; Conservative
                                                         Histone H1 (Fragment).
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                         STRAIN=Y;
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                         RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Aradon R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Bardon R.C., Baxer E.G., Helt G., Champo M., Ffeiffer B.D., R.A. Antil J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M., Ballew R.W., Bouch J.B., Burder J., Bander B., Botchan P., Brother B., Botchan M.R., Bouch J., Bayaktaroglu L., Beasley E.M., Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davise P., Andrews D., Botchan M.R., Bouch J., Bayara R.D., Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davise P., Anderson M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burtis K.C., Busam D.A., Baller C., Gabriellan A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P., Burtis N.L., Harvey D., Helman T.J., Herrisea S., Pleischman W., R.A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Kenniscon J.A., Ketchum K.A., Alash D., Houston K.A., Mixon K., Nussern D., Moshrefi A., Merkulov G., Mitchiel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A., Merkulov G., Mitchiel B.C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Whoshrefi A., Merkulov G., Milshina N.Y., Malssern D.M., Pletman G.S., Pan S., Pollard J., Put, Wang X., Merkulov G., Milshina N.Y., Malus F., Sanch H., Spier R., Schred R., Shue B.C., Stender K., Wassarman D.A., Mishorn M., Stung G., Zho Q., Zhan H., Spier R., Shrading A.C., Stapleton M., Stung G., Zho Q., Zhu S., Sho R., Shue B.C., Siden-Kamos I. Simpson M., Stung G., Zho Q., Zho Q., N. Wallew B.C., Stapleton M., Stung G., Zho Q., Zhu S., Shu B.C., Siden-Kamos 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbana T.T., Baxter E., Blazel R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M. Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.6%; Score 69; DB 5; Length 741; 61.3%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 741 AA; 84257 MW; 73D758634149385F CRC64;
                   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMB; TIGR00435; Cy8S; 1.
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Best Local Similarity 61.3
Matches 19; Conservative
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Gaps

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Score 68.5; DB 5; Length 83; Pred. No. 1.1; 3; Mismatches 12; Indels

41.3%;

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                                                                                                                                                                                                                                                                      Histone Hl protein.
Leishmania braziliensis.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Alonso V., Martinez B., Carmelo B., Pinero J., Gonzalez Alonso V., Martinez B., Carmelo B., Pinero J., Gonzalez Ortega A., Valladares B.;
"H1 from Leishmania braziliensis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131892; AAD26570.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; H1STONEH5.
SEQUENCE 112 AA; 11370 MW; 1657D5D106C2DB80 CRC64;
                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AKKSAPKKAVKKAVKAAKKAVKKAAK-KATKRTAKKAA 110
42 AKKRAAPKKKPAAAKKAVTKSAKKHAAKKAPKKAVKKA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKE-----KAAKKAYKKEAKAKAAEAAKEAA 32
                                                                                                                                               112 AA.
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                                                                                                                                               PRT;
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nes '21; Conservative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                            Q9XYY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                             RESULT 15
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:01 ; Search time 18.2384 Seconds
 (without alignments)
 255.712 Million cell updates/sec

US-09-816-989A-1

Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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| SIDS2/gcgdata/geneseq/geneseqp\_embl/AA1991\_DAT:\*
| SIDS2/gcgdata/geneseq/geneseqp\_embl/AA1991\_DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No. is the

### SUMMARIES

	Description	Copolymer molecula	C albicans apoptos	Recombinant copoly	Peptide modulating						
	ΩI		AAY82572	AAY82576	AAY82574	AAY82577	AAY82573	AAY82575	AAG70868	AAR06445	AAB08170
	DB	21	21	21	21	21	21	21	22	11	21
	e Match Length DB 1	35	45	98	99	109	26	77	427	154	40
* Query	Match	100.0	65.1	65.1	63.6	63.3	63.0	63.0	52.1	45.8	44.3
	Score	166	108	108	105.5	105	104.5	104.5	86.5	9/	73.5
Result	No.	т	7	m	4	S	9	7	80	σ	10

Recombinant copoly	Human protein segu	C glutamicum prote	Drosophila melanog	Polycationic polyp	Protamine-like pep	Peptide modulating	Polycationic polyp	Protamine-like pep	Drosophila melanog	ä	ω	ω	Arabidopsis thalia	Ø	Ø	Arabidopsis thalia	M. tuberculosis hi	$\overline{}$	Drosophila melanog		Drosophila melanog	2	Streptococcus pneu	Mycobacterium bovi	Enterococcus faeca	Enterococcus faeca	O			ņ	Polycationic polyp	Protamine-like pep	Protamine-like pep	T. cruzi L19E homo
AAR06446	AAM25508	AAG91997	ABB62028	AAR90180	AAW06686	AAB08168	AAR90181	AAW06688	ABB61894	AAU84310	AAG37166	AAG38490	AAG37165	AAG38489	AAG37164	AAG38488	AAY34055	AAY57353	ABB63417	AAY14928	ABB59960	AAG91846	AAW14537	AAB20575	AAU34982	AAU33397	AAY07029	ABB62173	ABB71574	AAR90176	AAR90178	AAW06687	AAW06697	AAW06913
11	22	22	22	16	18	21	16	18	22	23	21	21	21	21	21	21	20	21	22	20	22	22	18	21	22	22	20	22	22	16	16	18	18	11
106	146	165	741	32	32	32	33	33	515	582	242	242	245	245	300	300	214	214	481	223	322	498	203	205	169	782	621	607	2451	29	59	59	29	262
•	41.9	41.9	41.6	40.7	40.7	40.7	40.7	40.7	40.4	40.1	39.8	39.8	39.8	6	6	٥.	ο.	٥.	39.5	٥.	φ.	6	8	38.9	8	38.9	æ	•	æ	۲.	37.7	۲.	7	37.7
11	69.5	σ	69	67.5	67.5	67.5	67.5	67.5	67	66.5	99	99	99	99	99	99	S	65.5	65.5	65	65	65	4	4	64.5	4	n	63	63	ä	62.5	ď	ά.	. 62.5
11	12	13	. 14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

AAY82571 standard; peptide; 35 AA. 28-JUL-2000 (first entry) AAY82571; AAY8257. 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.

glatizamer acetate, autoimmune disease, antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid, antiinflammatory; antidiabetic; thyromimetic; haemostatic; antisporiatic; dermatory; antidiabetic; thyromimetic; haemostatic; antisporiatic; dermatory; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US22402. 24-SEP-1999;

98US-0101693. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Lis D;

Gad A,

98US-0101693

25-SEP-1998;

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune cuveoretinitis, crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psyndrome, Hashimoto's disease, with treated colitis, contact sensitivity disease, which can be treated in the collitis of the colitis of the collitis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                        Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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100.0%; Pred. No. 9.3e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular weight markers
                                                                                                                             WPI; 2000-317499/27.
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      Lis D;
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Gad A,
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1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 Query Match
Best Local Similarity 100.
Matches 35; Conservative ò 셤

AAY82572 standard; peptide; 45 AA 28-JUL-2000 (first entry) AAY82572; RESULT 2 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2. Copolymer; molecular weight marker; TV-marker; immune disease;

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteographic; immunosuppressive; antithyroid; antiinflammacory osteographic; thyromimetic; haemostatic; antiporniatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammacory condition; multiple sclerosis; theumatoid arthritis; crohi's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

WO200018794-A1 Unidentified

06-APR-2000.

99WO-US22402 24-SEP-1999;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune continued architic may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include architic conditions, canemia, autoimmune ophoritis, osteoarchritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia cuecretinitis, contact sensitivity disease, diabetes mellitus, Graves (Gisease, Guillain-Barres s syndrome, Hashimoto's disease, diabetes mellitus, contact sensitivity disease, diabetes mellitus, contact disease, diabetes mellitus, contact engitus etc. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to distant mer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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Pred. No. 6.7e-06;
1; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAEKAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.4
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular weight markers.
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AAY82576

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AAY82576 standard; peptide; 86 AA.

AAY82576;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronic immune thrombocycopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; penniqus vulgaris; systemic lupus erythematosus. 

Unidentified

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06-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopania purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.1%; Score 108; DB 21; Length 86; 57.4%; Pred. No. 1.3e-05; ive 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY82574 standard; peptide; 66 AA.
                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 14; 72pp; English.
                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                              99WO-US22402
                                                                                                                  98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.4
Watches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecular weight markers.
                                                                                                                                                                                                                                                        WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 AA;
WO200018794-A1
                                                                                                                                                                                                                     Lis D;
                                                                                                                  25-SEP-1998;
                                                                              24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000
                                    06-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or mithody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoria arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, choosic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          include host-versus-graft disease, graft-versus-host disease, and delayde-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 31; Gaps
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Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%; Score 105.5; DB 21;
43.9%; Pred. No. 1.9e-05;
iive 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317499/27.
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 EAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
                                                                                                                     Unidentified,
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AAY82573;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or conditions, damyellinating diseases. Such diseases include arthritic conditions, demyellinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune parent sease, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimcto's disease, and indopathic myxoedema, myasthenia gravis, psyndrome, Hashimcto's disease, and colled host-versus-graff disease, graff-versus-syraff disease, and celayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to an objecular weights and physical properties which are analogous to an objecular weights which makes them ideal for use as
                                      glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopethic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohr & disease; chronic immune thromboortopeania purpura; colitis; diabetes mellitus; draves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                    Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                               pemphigus vulgaris; systemic lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                             Unidentified
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7
                                                          Gaps
                                                        10;
                         63.3%; Score 105; DB 21; Length 109; 62.2%; Pred. No. 3.6e-05; ive 2; Mismatches 5; Indels 10
                                                                                      1 AKKYAKKEKAAKKAY----KKEA----KAKAAEAAKEAAYEA 35
                                                        Conservative
                                        Similarity
109 AA;
                                                       28;
Sequence
                          Query Match
Best Local 8
                                                        Matches
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for colypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple candental autoimmune obportitis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune haemolytic candental, autoimmune ophoritis, autoimmune thrombocytopaenia cuveoretinitis, contact sensitivity disease, diabetes mellitus, Graves copurar, colitis, contact sensitivity disease, diabetes mellitus, Graves (1 lupus erythematosus. Mediated-mediated diseases which can be treated conditioned host-versus-staft disease, gastemic disease, and disease, and defined molecular weights and physical properties of the invention have defined molecular weights and physical properties which are analogous to molecular mains and physical properties which mare analogous to molecular weights makes them ideal for use as

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AAY82573 standard; peptide; 56 AA.
                                AAY82573
ID AAY8
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7

21; Gaps

63.0%; Score 104.5; DB 21; Length 56; 51.8%; Pred. No. 2.1e-05; ive 4; Mismatches 2; Indels 21

29

1 AKKYAKKEKA----AKKAYKK-------EAKAKAABAAKBAAYBA 35

29; Conservative

Local Similarity

Best Loca Matches

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Query Match

56 AA;

Sequence

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glatitamer acctate; autoimmune disease, antiatthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoritatic; dermatory; antidabetic; thyrominetic; haemostatic; antipaoritatic; dermatory; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                               Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                          Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                       28-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Lis D;
                                                                                                                                                                                                                                                                                                  24-SEP-1999;
                                                                                                                                                                                                                       Unidentified.
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Weight TV-marker polypeptides from the present invention. The present weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated of the diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune baemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune vecetinitis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimoto's disease, indepathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to mylerniar weights molecules, which makes them ideal for use as
                                                                                                                                                                                                                      Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
                                          AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lis D;
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                                                                                        AAY82575;
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                AAY8257
RESULT
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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 427;
                                                                                                                                                                                                        Yeast, fungus, apoptosis, infection, proliferative disease, vaccine, autoimmune disease, ischaemia, neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                       Luyten WHML, Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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35
              40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB .02;
                                                                                                                                                                              C albicans apoptosis associated protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 KEKAKKEKAAKKWEKESGSRKAAEEAAKKAAEEA 317
 1 AKKYAKKEKAAKKAY---KKEAKAKAAEAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.02
3; Mismatches
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Pred. No. 0.
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                                                                                              AAG70868 standard; Protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                     De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f match 52.1%;
Local Similarity 65.7%;
les 23; Conservative 3
                                                                                                                                                                                                                                                                                                                                    03-JUL-2000; 2000WO-BE00077.
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                                                                                                                                                  27-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         (JANC ) JANSSEN PHARM NV.
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N-PSDB; AAH29904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AA;
                                                                                                                                                                                                                                                  Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 certain diseases
                                                                                                                                                                                                                                                                              WO200102550-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Contreras RH,
Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                                               01-JUL-1999;
                                                                                                                                                                                                                                                                                                        11-JAN-2001
                                                                                                                          AAG70868;
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Matches
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Gaps

3;

63.0%; Score 104.5; DB 21; Length 77; 65.8%; Pred. No. 2.9e-05; ive 4; Mismatches 6; Indels 3.

25; Conservative

Matches

Query Match Best Local Similarity

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The present sequence represents a synthetic peptide which has a high affinity for glycoaminoglycans and proteoglycans. The peptide is useful in methods for modulating heparin or other glycoaminoglycans with anticoagulant activity, promoting cell attachment or adhesion to natural or synthetic surfaces (especially vein grafts), modulating curfunds differentiation, targeting drugs to epithelial cell surfaces (or to other cells expressing proteoglycans), modulating enzymes that act on glycoaminoglycan elfinity purification of bioactive sequences of a glycoaminoglycan, modifing endethelial cell pro-coagulant or anti-coagulant functions mediated through glycoaminoglycans, and inclusing endethelial cell pro-coagulant or anti-coagulant functions mediated through glycoaminoglycans, and tissue uptake of heparin or other glycoaminoglycans in a mammal to increase heparin half-life in circulation.
                                                                                                                                                                                                                                                                                                                                 Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumour metastasis and modulating wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copolymer 1; COP-1-19; myelin basic protein; MBP; il activity; autolmmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.3%; Score 73.5; DB 21; Length 40; 61.1%; Pred. No. 0.061; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KKAAKAARKKAAKKAARKKAARKKAAKAARKKAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAK--KEKAAKKAYKKEAKA---KAAEAAKEAA 32
                                                                                                                                                                                                                                                  Schick BP;
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                                  Verrecchio A,
                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                             99US-0118276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0312541.
                                                                                                              02-FEB-2000; 2000WO-US02853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0473845,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 61.1 tes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                              WPI; 2000-543446/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunological activ
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 AA;
                                                                                                                                                                                                                                                  San Antonio JD,
                         WO200045831-A1
                                                                                                                                                             02-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant
                                                                     10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06446
    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. C the COP-1 polypeptide may be cleaved from the fusion protein. I cOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, ERK, KAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleaved of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitias. They are used to prevent, arrest or control a cerephalomyelitiae. They are used to prevent, arrest or control a be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant; cell attachment; cell adhesion; vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide modulating activity of heparin, and other glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 KKKAKEAEKAKKAKKKKKKKKEAEAAKAAKAAAAAYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.8%; Score 76; DB 11
54.1%; Pred. No. 0.12;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB08170 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match. 45.8%;
Best Local Similarity 54.1%;
Matches 20; Conservative
                                                                                                                                                                                                                           90EP-0301700.
                                                                                                                                                                                                                                                                     90US-0473845.
89US-0312541.
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                                                                                                                                                                                                                                                                                                                                     (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       certain amino acids
                                           multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ05664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ05665
                                                                                                                                                                                                                           16-FEB-1990;
                                                                                                                                                                                                                                                                                              17-FEB-1989;
                                                                                                                                                                                                                                                                       07-FEB-1990;
                                                                                                                                                                               22-AUG-1990
                                                                                                                                 EP383620-A.
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                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Cook KS;
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RESULT 10 AAB08170 ID AAB0

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7

Gaps

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Tang YT, Liu C, Drmanac RT

(HYSE-) HYSEQ INC.

2001-457603/49.

N-PSDB; AAH99449

23.DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317.

22-DEC-2000; 2000WO-US35017.

26-JUL-2001.

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Human, cancer; ulcer, HIV infection; human immunodeficiency virus;
antibacterial; endocrine; cardian; central nervous system; virucide;
antibacterial; endocrine; cardian; central nervous system; virucide;
antibacterial; endocrine; cardian; cardiavascular; antibacterial; antibacterial; endocrine; cardian; cardiavascular; antibacter; antibacter; antibactic; enzema;
antiaggregant; haemostatic; vulnerary; antibloer; osteopathic; eczema;
dermatological; antialergic; antiathmatic; cytostatic;
neuroprotective; antidepressant; nootropic; antidabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antidabetic; cytostatic;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoloid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropachology; cardiac anaphylaxis; autoimmunity;
genetic disease; heematopoietic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                 coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleocited duplexes incoding the following segments: YKK, AAE, KAK, EKA, KKA, YEA, AKA KEA, and AAA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control sdemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                              Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.8%; Score 71; DB 11; Length 106;
48.9%; Pred. No. 0.32;
ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                               To improve the expression of rCOP-1 polypeptides in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:1023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM25508 standard; Protein; 146 AA
                                                                                                                                                                                                                        Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KYAKKEKAAKKAYKKE-AKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 48.9
1es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorder.
                                                                WPI; 1990-255848/34.
N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAQ05664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                    Cook KS;
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Matches
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                                                                                      Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                          ..
2
                                                                                                                                                                                                                                                       y match
Local Similarity 52.6%; Pred. No. 0.65;
hes 20; Conservative
                                                                                                                                                                                                                                                                                            C glutamicum protein fragment SEQ ID NO: 5751.
                                                                                                                                                                                                                                                                                      3 KYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYEA
                                                                                                        Claim 20; Page 210; 1217pp; English.
                                                                                                                                                                                                                                                                                                                              AAG91997 standard; Protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                       neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                   organic acid synthesis.
                                                                                                                                                                                                                                                   Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         EP1108790-A2.
                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2001
                                                                                                                                                                                                                                                                                                                                          AAG91997;
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                   RESULT 13
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher everaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                              Disclosure; SEQ ID NO 12876; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                   41.6%; Score 69; DB 22; Length 741; 61.3%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                          649 AKLAABAEKAAAEKERKKQAAAEA--AAAKEA 677
                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEA 31
                                                                                                                                                                                                                                                                                                                                                  19; Conservative
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 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-193899/25.
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                       (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                          741 AA;
WPI; 2001-656860/
N-PSDB; ABL06131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9513083-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR90180;
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
 à
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitemins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office.
                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 23
                                                                                                                                                                                                                                                 Claim 17; SEQ ID NO: 5751; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 165;
                                                                                             Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 12876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KKKAREDKEAKEAAEKAAAEKAAAAESEEAPAEEAAAE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKYAKKEKAAKKAYKKEAKAKAA-----EAAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69.5; DB Pred. No. 0.74; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB62028 standard; Protein; 741 AA
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                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%;
                         07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
              99JP-0377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0°
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                       2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 AA;
                                                                                                                                                    N-PSDB; AAH67216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
              16-DEC-1999;
                                                                                             Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB62028;
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Gaps

2,

Indels

; 9

4; Mismatches

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New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing low mol.wt.
                                                                                                                                                                                                         n-protamine, anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                       'note= "N-terminal is acetylated"
                                                                                                                                                               Polycationic polypeptide n-protamine analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wakefield
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 13; 34pp; English
     Ą.
AAR90180 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0303025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US12981
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanley JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heparin anticoagulation
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Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids articular the peptides evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-proteamine (total cationic charge = +21) in which selected arginine residues have been replaced by other positively charged amino acids and other arginine residues have been replaced by other positively charged amino acid residues have been replaced by other positively charged amino acid residues, breferably lysine. The peptides reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action.

The present sequence (total cationic charge = +18) is a specific example of the new polypeptides. 

32 AA; Sequence

ä Gaps 1, Query Match
40.7%; Score 67.5; DB 16; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.24;
Matches 19; Conservative 2; Mismatches 9; Indels 1

1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30 2 AKKAAKKAKKAKKAKKAKKAKKAXKAXKX 32 ò g

Search completed: March 10, 2003, 12:21:27 Job time : 19.2384 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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March 10, 2003, 12:26:10 ; Search time 10.4114 Seconds (without alignments) 141.764 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-816-989A-1 Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188354 segs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:\*
2: /cgn2\_6/ptodata/1/pubpaa/PUB.WB PUB.pep:\*
3: /cgn2\_6/ptodata/1/pubpaa/BOOF NEW PUB.pep:\*
4: /cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
6: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
7: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
9: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
9: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
10: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/1/pubpaa/USO0\_NEW PUB.pep:\*
14: /cgn2\_6/ptodata/1/pubpaa/USO0\_NEW PUB.pep:\*
14: /cgn2\_6/ptodata/1/pubpaa/USO0\_NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 1, Appli	_	9	Sequence 4, Appli	7	Sequence 3, Appli	, ,	Sequence 8, Appli	~	Sequence 100, App			Sequence 10575, A	Sequence 4893, Ap	Sequence 7, Appli	Sequence 24, Appl	Sequence 27, Appl	Sequence 9, Appli	
ΩI	US-09-816-989A-1	US-09-816-989A-2	US-09-816-989A-6	US-09-816-989A-4	US-09-816-989A-7	US-09-816-989A-3	US-09-816-989A-5	US-09-820-843A-8	US-09-738-626-5751	US-09-919-497-100	US-10-051-643-201	US-09-738-626-5600	US-09-815-242-10575	US-09-815-242-4893	US-10-093-892-7	US-09-820-843A-24	US-09-820-843A-27	US-10-093-892-9	US-10-093-892-5
DB	101	10	10	10	10	10	10	6	σ	10	6	σ	10	10	δ	0	6	σ	σ
* Query Match Length DB	35	45	96	99	109	56	77	372	165	582	223	498	169	782	96	309	356	96	105
& Query Match	.100.0	65.1	65.1	63.6	63.3	63.0	63.0	44.6	41.9	40.1	39.5	39.2	38.9	38.9	37.3	37.0	35.8	35.5	35.5
Score	166	108	108	105.5	105	104.5	104.5	74	69.5	66.5	65	65	64.5	64.5	62	61.5	59.5	59	59
Result No.		7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

20 59 35.5 890 10 US-09-815-242-10314 22 3 34.3 102 9 US-09-999-724-90 23 34.3 18 9 US-09-999-724-90 23 34.3 31.8 9 US-09-999-724-90 25 57 34.3 352 9 US-09-999-724-46 25 56 33.7 300 10 US-09-995-724-46 25 56 33.7 300 10 US-09-915-242-13765 26 33.7 4 20 10 US-09-815-242-13765 29 E5.5 33.4 200 10 US-09-815-242-13765 29 E5.5 33.4 200 10 US-09-815-242-1235 31 E5.5 33.1 89 10 US-09-864-761-45765 31 E5.5 33.1 89 10 US-09-864-761-45765 31 E5.5 33.1 150 10 US-09-864-761-45765 31 E5.5 33.1 150 10 US-09-864-761-45765 31 E5.5 33.1 369 9 US-09-864-761-45765 31 E5.5 284 9 US-10-141-627-4 41 E5.5 284 9 US-10-141-627-6 41 E5.5 284 9 US-09-864-187 E5.5 31 E5.5 31 US-09-864-186-187 E5.5 31 E5.5 31 US-09-864-187 E5.5 31 E5.5 31 US-09-864-186-187 E5.5 31 E5.5 31 US-09-864-187 E5.5 284 9 US-09-964-187 E5.5 284 9 US-09-864-187 E5.5 284 9 US-09-864-187 E5.5 284 9 US-09-864-187 E5.5 284 9 US-09-964-184 E5.5 285 284 9 US-09-964-184 E5.5 285 284 9 US-09-964-184 E5.5 285 284 9 US-09-964-1
83 88 88 88 88 88 88 88 88 88 88 88 88 8
80 00 00 00 00 00 00 00 00 00 00 00 00 0
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#### ALIGNMENTS

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK!

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

THE REPREMENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: PT/US99/22402

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PALENTIN VERSION 3.1

LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1
Sequence 1, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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ö Length 35; Indels Query Match 100.0%; Score 166; DB 10; Best Local Similarity 100.0%; Pred. No. 2.4e-13; Matches 35; Conservative 0; Mismatches 0;

ö

## 1 AKKYAKKEKAAKKAYKKEAKAKAABAAAKEAAYEA 35 ð g

1 AKKYAKKEKAAKKAYKKEAKAKAABAAKEAAYEA 35

Sequence 2, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION: APPLICANT: Gad, Alexander APPLICANT: Lis, Doris US-09-816-989A-2

1;

Gaps

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Sequence 7, Application US/09816989A
; Sequence 7, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
    APPLICANT: Lis, Doris
    APPLICANT: Lis, Doris
    TILLE OF INVENTION: COOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
    TILLE OF INVENTION: AND FOR THERAPEUTIC USE
    FILE REFERENCE: 2609/60807-A-PCT-US
    CURRENT PRILING DATE: 2001-03-23
    FILE REPLICATION NUMBER: 60/101,693
    PRIOR FILING DATE: 1999-09-25
    PRIOR PILING DATE: 1999-09-24
    NUMBER OF SEQ ID NOS: 7
    SEQ ID NO 7
    SEQ ID NO 7
    LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09816989A

PREFAIT NO. US2020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

ITILE OF INVENTION:

TITLE OF INVENTION:

AND FOR THERAPEUTIC USE

TITLE OF INVENTION:

AND FOR THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KAKAAEAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAAKKAY----KKEA----KAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 63.3%; Score 105; DB 10; 1 Similarity 62.2%; Pred. No. 8.8e-06; 28; Conservative 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 105.5; DB 10
43.9%; Pred. No. 4.5e-06;
live 2; Mismatches 4;
      CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 4
LENGTH: 66
LENGTH: 66
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAAKKAYKKEA------
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.6
Best Local Similarity 43.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 28; Conserva
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US-09-816-989A-7
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US-09-816-989A-3
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT PILLNG DATE: 2001-03-23 PRIOR PILLNG DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PSEC ID NOS: 7 SEQ ID NOS: 7 SEG ID NOS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERABEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PILING DATE: 12001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7,507. Application US/09816989A

Patent No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FIGER REFERENCE: 2609/60807-A-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 10;
Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 108; DB 10;
Pred. No. 1.6e-06;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.1%;
Best Local Similarity 64.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-816-989A-4
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Patent No. US20020106662A1

GENERAL INFORMATION

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REPREMENCE: B00801/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                          DB 9; Length 372;
                                                                                                                                                               CTHER INFORMATION: outer membrane integrity protein (tola)
NAME/KBY: misc feature
CTHER INFORMATION: gi | 1573353
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAAKKAYKKEAKAKAA----EAAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO STSI
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
44.6%; Score 74;
Best Local Similarity 58.1%; Pred. No. (
Matches 18; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                5 AKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5751, Application US/09738626
Publication No. US20020197605A1
GENERAL INPORMATION:
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       j ORGANISM: Corynebacterium glutamicum
US-09-738-626-5751
            SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                          TYPE: PRT
ORGANISM: H. influenzae
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-919-497-100
                                    SEQ ID NO 8
LENGTH: 372
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APPLICANT:
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; Patent No. US20020115103A1
; GENERAL INPORMATION:
APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT APPLICATION NUMBER: 60/101,693
; PRIOR PILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR PILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Version 3.1
; SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USFFUL AS ANTI-INFECTIVES
FILE REPRENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
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                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKA----AKKAYKK-----BAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 104.5; DB 10;
Pred. No. 5e-06;
4; Mismatches 2; :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 104.5; DB
Pred. No. 7e-06;
4; Mismatches
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
FRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.0%;
65.8%;
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.0%;
Best Local Similarity 51.8%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 65.8
Matches 25; Conservative
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US-09-816-989A-5
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US-09-820-843A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10575, Application US/09815242

Sequence 10575, Application US/09815242

Releant No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Wall, Danial D.

APPLICANT: Wall, Danial D.

APPLICANT: Wannoro, Robert T.

APPLICANT: Wannoro, Robert T.

APPLICANT: Xu, H. Howard

ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: DENCARYOTES

FILE REPERENCE: ELITRA, 01A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-10-26

PRIOR PILING DATE: 2000-10-27

PRIOR PILING DATE: 2000-10-26

PRIOR PILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO 10575

LENGTH: 769
                                                                                                                                                                                                                                                                                                                        Query Match 39.2%; Score 65; DB 9; Length 498; Best Local Similarity 53.3%; Pred. No. 1.8; Matches 16; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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38.9%; Score 64.5; DB 10;
Best Local Similarity 48.6%; Pred. No. 3.3;
Matches 17; Conservative 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAK-KEKAAKKAYKKEAKAKAAEAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 AKKTARKAPAKKTVAKKATTAKAAPATAKD 113
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 5600
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Enterococcus faecalis
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US-09-815-242-4893
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ORGANISM:
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Sequence 201, Application US/10051643

Sequence 201, Application US/10051643

Sequence 201, Application US/10051643

Sequence 201, Application US/20020197265A1

Seturation No. US20020197265A1

APPLICANT: Watson, James D.

APPLICANT: Watson, James D.

TITLE OF INVENTION: Paul L. J.

TITLE OF INVENTION: System using Mycobacterium Vaccae

TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REPERENCE: 11000-100802

CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT FILING DATE: 1098-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 201

LENGTH: 223
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                 40.1%; Scc. 10. 1... 48.6%; Pred. No. 1... 7; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                 295 KKFKEEEKAKKEAEKKAKAEAKRKEQEAKEKOROA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAAKKAYKK-EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
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FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 100
LENGTH: 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5600, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: O'CHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: INTERNI, NAOKO
APPLICANT: INTERNI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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US-09-738-626-5600
                                                                                                                                                                                                  US-09-919-497-100
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TITLE OF INVENTION: IMMUNITY TO TRYPANOSOMATIDS SPECIES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: 91118bury Madison & Sutro
STREET: 1100 New York Avenue, N.W.
                                                                                                                        APPLICANT: Haselbeck, kobetch
APPLICANT: Ohlsen, Kari L.
APPLICANT: 29kihid, Judith W.
APPLICANT: 29kihid, Judith W.
APPLICANT: 29kihid, Judith W.
APPLICANT: Amamoto, Mobit D.
APPLICANT: Carr, Grant J.
APPLICANT: Amamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILES REFERENCE: ELITAN.011A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-11-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
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PRIOR PLING DATE: 2001-12-3
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PRIOR PLING DATE: 2001-03-3
PRIOR PLING DATE: 2001-03-3
PRIOR PLING DATE: 2001-03-3
PRIOR PLING DATE: 2001-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAK-KEKAAKKAYKKEAKAKAAEAAAKEAAYE 34
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APPLICATION NUMBER: US/10/093,892
FLLING DATE: 11-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10093892
Patent No. US/20020177697A1
GENERAL INFORMATION:
APPLICANT: FASEL, Nicolas Joseph
Sequence 4893, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecalis US-09-815-242-4893
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                                                                                                                APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.9
Best Local Similarity 48.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-10-093-892-7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                               REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 11422/224090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFRAX: 202-862-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKK--EKAAKKAYKKEAK--AKAAEAAKEA 31
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        APPLICATION NUMBER: EP 96200665.6
APPLICATION NUMBER: EP 96200665.6
US/08/668,255
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: March 10, 2003, 12:53:42 Job time: 10.5543 secs
                                                                                                                                                                                                                                                                                      LENGTH: 96 amino acids
                                                      FILING DATE: March 12,
ATTORNEY/AGENT INFORMATION:
NAME: Paul N. Kokulis
                                                                                                                                                                                                                                                                                                                                                                                                        37.3%;
57.1%;
                                                                                                                                                                                                                TELEX: 6714627
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 20; Conserv
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(without alignments)
166.029 Million cell updates/sec
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                                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                            166
1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
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US-08-303-025-15
US-08-436-7038-2
US-08-436-7038-4
US-08-436-7038-4
US-08-436-7038-4
US-09-095-855-201
US-08-152-488-11
US-08-152-488-11
US-08-152-488-11
US-08-303-025-11
US-08-436-7038-3
US-08-436-7038-3
US-08-436-7038-15
US-08-436-7038-15
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: RM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEPAX: 908-276-5543
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: N/A PUBLICATION INFORMATION: AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                               US-08-677-304-13
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40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.05;
Matches 19; Conservative 2; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY.
CITY: Detroit
STATE: Michigan
COUNTRY: Databal
ZIP: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 313-496-4545
INFORMATION FOR SED ID NO: 15:
FENDERAL 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Benita J, Rohm, Esg.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                  1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                             2 AKKAAKKAKKAKKAKKAAKKAKAKK 32
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-13
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; FILING DATE: 14-AUG-1993
US-08-303-025-15
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08303025
Patent No. 5614494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDENNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
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Sequence 13, Application US/08677304
Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: AAACEWS, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
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40.7%; Score 67.5; DB 1;
Best Local Similarity 61.3%; Pred. No. 0.05;
Matches 19; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
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CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08669
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                           NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDENDESS: No. 5721212 Relevant TOPOLOGY: No. 5721212 Relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-436-703B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Makefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Standey, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE Benita J, Rohm, Esq.
STREET: 6611 Woodward Avenue
STREET: Suite 1525
                                                                                            STREET: 150 WEST DETECTION, SUITE 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORY diskette 3.5" 1.44Mb
COMPUTER: DEAD COMPATIBLE
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WOTAGEFIECT 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AuG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Bentia J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-16
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; Sequence 4, Application US/08436703B
; Patent No. 5919761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N/A
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Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                    APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: WRIGHT HEPARIN
TITLE OF INVENTION: WRIGHT HEPARIN
TITLE OF INVENTION: WISCHEL HEPARIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7WK-060548-00233
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 6;
SOFTWARE: MSCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AKKAAKKAKKAAKKAAKKAKKAKKA32
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                                                                                                                                                                                                                                                                                                                                                                                      CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
Sequence 2, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFTCATION: 514
CLASSIFTCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REPERENCE/DOCKET NUMBER: 74K-(TELECOMMUNICATION INFORMATION:
TELEFAX: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TITLE: N/A
US-08-436-703B-2
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US-08-303-025-16
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Gaps

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Query Match 39.5%; Score 65.5; DB 3; Length 214; Best Local Similarity 52.4%; Pred. No. 0.63; Matches 22; Conservative 3; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTIER READABLE FORM:

MEDIUM TYPE: Disketter
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: DISKETED
COPERATING SYSTEM: DOS
SOFTWARE: FASESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 21-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCEY/DOCKET NUMBER: 11000.1002c3
TELLEPHONE: 206-269-0565
                                        NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPAS: (619) 535-9001
TELEPAS: (619) 535-9001
TELEPAS: (619) 535-9949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
FILING DATE: 11-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-041-889-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-095-855-201
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Patent No. 6033864
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4330 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

40.7%; Score 67.5; DB 2; Length 33;
Best Local Similarity 61.3%; Pred. No. 0.051;
Matches 19; Conservative 2; Mismatches 9; Indels
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STREET: 4370 La Jolla Village Drive, Suite 700
STATY: San Diego
STATY: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/837,058
          COMPUTER REALBELE FORM;
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MordPerfect 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROIM, Benita J.
RECISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-0023:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 4
SEQUENCE FRARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TITLE: N/A
US-08-436-703B-4
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37.7%; Score 62.5; DB 1; Length 29; 62.1%; Pred. No. 0.17; tive 1; Mismatches 9; Indels
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Fatent No. 5534619
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
SIATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILLING DATE: 12-NOV-1993
          WordPerfect 6; ASCII (DOS) Text
                                                                        PELLICATION: FILING DATE: TELLING DATE: TELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAYKKEAKAKAAEAAK 29
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                                                       UMBER: US/08/152,488
12-NOV-1993
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COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORGINAL SOURCE: peptide
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.18
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-152-488-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nation, 100.
APPLICANT: ARISON, Compounds and Methods for Treatment and TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4
CURRENT FILING DATE: 1999-12-04
CURRENT FILING DATE: 1998-12-04
EARLIER PILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE PERSEQ for Windows Version 3.0
                                                                                                                                          DB 4; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 4; Length 223; Pred. No. 0.75;
                                                                                                                                                                                                        10; Indels
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Patent No. 5534619
GENERAL INFORMATION:
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION:
ITTLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN ITTLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
                                                                                                                                      Score 65; DB 4;
Pred. No. 0.75;
4; Mismatches
                                                                                                                                                                                                                                                                                                               112 ARKAAKKAPAKKAAAKKAAPAK--KAPAKKAATKA 144
                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
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COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 201, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQ ID NO 201
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.2%;
                                                                                                                                   Query Match
Best Local Similarity 54.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-205-426-201
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US-08-152-488-10
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Gaps
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                                                                                                                                                                                                                                                                                                                          Query Match 37.7%; Score 62.5; DB 1; Length 29; Best Local Similarity 62.1%; Pred. No. 0.17; Matches 18; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 150 west collection:

STATE: Michigan
CONTRY: United States of America
ZIP: 48226-4415
COMPUTER: Eloppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: WordPerfect 6.1; ASCII (DOS) Text
COMPUTER: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION NUMBER: PCT/US92/06829
FILING DATE: 14-NUG-1992
APPLICATION NUMBER: DCT/US92/06829
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM BEATLE J.
TELEFORM BEATLE J.
TELEFORM SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
STRANDENESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AKKAAKKAAKKAKKAAK-KAKKAAKK 29
                                                                                                                                       ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
ITILE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILLING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
                          TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
         29 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: N/A .
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-303-025-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08303025
Patent No. 564494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDERS:
ADDRESSE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Detroit
STATE: Michigan
COUNTY: Detroit
ZIP: 4826-4415
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: READABLE FORM:
MSDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IRM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CCASSIFTCATION: S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm. Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7WH-060548-00231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AKKAAKKAAKKAKKAAK-KAKKAAKK 29
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPRONE: 908-276-3344
TELEPRONE: 908-276-5543
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
IS-08-152-488-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                            ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 3:
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                            TITLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-303-025-10
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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tive 1; Mismatches 9; Indels
                                                                                                                                                     Sequence 10, Application US/08677304

Patent No. 5721212

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
ITILE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES:
ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 6; ASCII (DOS) Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALL...

PILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATONNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
FERRENCE/DOCKET NUMBER: RA-7WG
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
       1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                               AKKAAKKAKKAAKKAAK-KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 10, 2003, 12:30:01 Job time : 7.20253 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAAKKAYKKEAKAKAAEAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AKKAAKKAKKAKKAKKAAK - KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
US-08-677-304-L0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEEEPHONE: 908-276-3344
TELEPAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.1?
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N/A
                                                                                                                    RESULT 15
US-08-677-304-10
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                                                                                                                                                                    Gaps
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                                                                                                               37.7%; Score 62.5; DB 1; Length 29; 62.1%; Pred. No. 0.17;
                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY.

CITY.

CITY.

CONTRY: United States of America

ZIP: Michigan

COMPUTER: Michigan

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb

COMPUTER: LEM PC compatible

COMPUTER: MordPerfect

COMPUTER: WordPerfect

COMPUTER: WordPerfect

COMPUTER: WordPerfect

COMPUTER: MordPerfect

COMPUTER: MordPerfect

CURRENT APPLICATION DATA:

PRICED DATE: 08-SEPT-1994

CLASSIFICATION NUMBER: US/08/303,025

FILING DATE: 14-AUG-1992

RPPLICATION NUMBER: US/08/152,488

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231

TELECOMMUNICATION INFORMATION:

TELECHONE.

TELECHONE: 313-496-7622
                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Benita J, Rohm, Esq.
150 West Jefferson, Suite 2500
                                                                                                                                                                                                          1 AKKYAKKEKAAKKAYKKEAKAKAAEAAK 29
                                                                                                                                                                                                                                      2 AKKAAKKAAKKAAKKAAK-KAKKAAKK 29
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-13
                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acids
STRANDEDNESS: N/A
                                                                                                                                                             Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.7
Best Local Similarity 62.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 150
CITY: Detro
                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-303-025-13
                                                                                                                  Query Match
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Compugen Ltd.
GenCore version (c) 1993 - 2003
           Copyright
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protein search, using sw model OM protein

Run on:

March 10, 2003, 12:15:04 ; Search time 13.1862 Seconds (without alignments) 327.825 Million cell updates/sec

Title: Perfect score:

US-09-816-989A-2 213 1 AKKYAKKAKAEKAKKAYKAA.....AKYEKAAAEKAAAKEAAYEA 45 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

probable rotamase hypothetical prote	histone H1 - Chlam	histone H1 - tomat	polyhydroxyalkanoa	tolA protein [impo	histone H1.10 - ch	histone H1-5 (vali	invariant surface	probable transfera	histone H1A - Afri	histone H1-II - Vo	TolA colicin impor	ribosomal protein	hypothetical prote	histone H1 - mouse
A81794 S29309	859589	845662	G83013	AG0592	A28456	S51660	B38145	B70868	151227	JN0748	AC0138	JC5954	T06636	A28470
01 01	~	N	7	N	N	н	~	~	7	~	N	N	~	N
347	231	287	309	376	220	226	523	580	229	241	388	220	924	212
37.1	36.6	36.6	36.6	36.4	36.2	36.2	36.2	36.2	35.7	35.7	35.7	35.4	35.4	35.2
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79	78	7	•	77.5								75	75	

### ALIGNMENTS

A2550 histone Hl - sea urchin (Lytechinus pictus) C.Species: Lytechinus pictus (painted urchin) C.Spate: 30-Jun\_1988 #sequence\_revision 30-Jun-1988 #text\_change 23-Jul-1999

C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Rvacleic Acids Res. 14, 8121-813, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Accession: A25550

A;Molecule type: DNA A;Residues: 1-210 <KNO> A;Cross-references: GB:X0488; NID:g9616; PIDN:CAA28177.1; PID:g9617 C;Superfamily: histone H1 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus

Gaps ä Length 210; Indels Score 103.5; DB 2; Pred. No. 0.0053; 3; Mismatches 11; 48.6%; Query Match Best Local Similarity 65.11 Matches 28; Conservative

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166 AKKAAKKPAAKKPAKKPAAKKPAAKKAAKPAAKKAA 208 1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42 셤 ઠ

RESULT 2

membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain i C;Species: Escherichia coli (5Pecies: Escherichia coli (5Peciesion: Esporas 18-701-2001 (5Peciesion: Espo

A, Residues: 1-394 <HAY>

A,Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A,Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A,Gene: EC80774

Gaps ; 9 Query Match

46.0%; Score 98; DB 2; Length 394;
Best Local Similarity 65.3%; Pred. No. 0.028;
Matches 32; Conservative 2; Mismatches 9; Indels

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Abjoint in protein in mol941 [imported] - Listeria monocytogenes (strain EGD-e) C; Species: Listeria monocytogenes C; Accession: Abio-2001 C; Amend, A.; Baquero, F.; Berche, P.; Bloecker. J.; Doninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Maltournam, A.; May A; Cschlueter, T.; Simces of Listeria species. A; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Accession: AB1317 A; Status: preliminary A; Status: preliminary A; Coss-references: GB:NC_003210; PIDN:CAD00019.1; PID:g16411394; GSPDB:GN00177 A; Csparimental source: strain EGD-e C; Genetics: A; Genetics: G
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Cispecies: Listeria incora
Cispecies: Listeria in Euchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
Cispecies: Listeria in Euchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Reference number: AB1077; WUID:21537279; PMID:11679669
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A;Experimental source: strain Clip11262
C;Genetics:
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1 AKKYA-KKAKAEKAKKAYKAAEAKKA-
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Best Local Similarity
Matches 27; Conserva
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A,Molecule type: DNA
A,Residues: 1-243 <GLA>
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                                                                                                                                                                                                                             membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: 16-F8b-2001 #sequence_revision 16-F8b-2001 #text_change 09-Nov-2001
C;Accession: G85576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: G85576
A;Status: preliminary
A;Motcession: G85576
A;Status: preliminary
A;Motcession: G85576
A;Status: cferences: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09
A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z05
C;Genetics:
A;Gene: tolA
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JV0057

CJOA protein - Escherichia coli (strain K-12)

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002

C;Datesion: JV0057; Bsd810

R;Levengood, S.K.; Webster, R.E.

J. Bacteriol. 171, 6600-6609, 1989

A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ

A;Reference number: JV0057; MUID:90078104; PMID:2687247
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C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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A, Residues: 1-421 < LEVA
A, Residues: 1-421 < LEVA
A, Residues: 1-421 < LEVA
A, Crossion and Local surgals and Local 
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KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 267
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A; Residues: 1-421 <BLAT>
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A; Start codon: GTG
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Matches 32;
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220
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DNA topoisomerase I [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87553
R;Accession: B87553
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Title: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum Th
A;Reference number: A43592; MUID:91372983; PMID:1894368
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: G70673 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-214 <COL>
                                                                                                                                                                                                                                                  A; Cross-references: GB: Z83018; GB: AL123456; NID: g3261671; PIDN: CAB05427.1; PID: g1694845
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A;Cross-references: GB:MS8563; NID:g155066; PIDN:AAA27480.1; PID:g155067
A;Note: the authors translated the codon TTC for residue 316 as Tyr, and CGA C;Keywords: membrane protein
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C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: B43592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DB 2; Length 214;
Pred. No. 0.11;
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5; Mismatches
                                                                                                                                                                                                                                                                                        A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%;
Matches 25; Conservative
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A;Gene: hupB
C;Superfamily: histone H1
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Matches
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histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
C;Accession: A28100
R;Lai, C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable hupB - Mycobacterium tuberculosis (strain H37RV)
[Species: Mycobacterium tuberculosis
[Species: Mycobacterium tuberculosis
[Spacies: Nycobacterium tuberculosis
[Spacies: Nycobacterium tuberculosis
[Spacies: Nycobacterium tuberculosis
[Spacies: Nycobacterium tuberculosis
[Spacies: Nycopacies: Nyco
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                                                              Sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Accession: S51364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Bur. J. Biochem. 255; 10894
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif r lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei. A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
A;Status: nucleic acid sequence not shown
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.3%; Score 90; DB 2; Length 1390;
57.8%; Pred. No. 0.41;
tive 4; Mismatches 11; Indels
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Pred. No. 0.11;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1390 «NEE>
A; Cross-references: EMBL:X73481
R; Neesen, J; Heinlein, U.A.O.; Buenemann, H.
B; Reference number: S34153
A; Reference number: S34153
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Matches 26; Conservative
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A;Molecule type: DNA
A;Residues: 1-211 <LAI>
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A;Gene: mst101(2)
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A;Residues: 'X',3-39 <SCA2>
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C,Superfamily: histone H1
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                                                                                                                                                                                                     hypothetical protein Rv0475 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R;Stcover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S*;; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
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A;Residues: 1-199 <COL>
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S34153
mst101-1 protein - fruit fly (Drosophila hydei)
mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34153
R;Nessen, J.; Heinlein, U.A.O.; Buenemann, H.
R;Nessen, J.; Heinlein, U.A.O.; Buenemann, H.
A;Reference number: S34153
A;Reference number: S34153
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-344 <NES>
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40.4%; Score 86; DB 2; Length 344;
Best Local Similarity 57.8%; Pred. No. 0.33;
Matches 26; Conservative 3; Mismatches 12; Indels
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                                   1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
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Pred. No. 0.21;
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A,Gene: FlyBase:Dhyd/mst101
A,Cross-references: FlyBase:FBgn0011816
C,Superfamily: neurofilament triplet H protein
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Best Local Similarity 65.6%;
Matches 21; Conservative 4
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Recession: E83525
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-347 <STO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001:A;Experimental source: strain PA01
A;Experimental source: strain PA01
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histone HI homolog - Bordetella pertussis
histone HI homolog - Bordetella pertussis
C;Species: Bordetella pertussis
C;Species: Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 23-Uul-1996. #sequence revision 06-Sep-1996 #text_change 24-Nov-1999
C;Accession: S61926; S69327
R;Scarlato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R., Mol. Microbiol. 15, 871-881, 1995
A;Title: A novel chromatin-forming histone HI homologue is encoded by a dispensable and cince number: S61926; MUID:95319329; PMID:7596289
A;Accession: S61926
A;Molecule type: DNA
A;Ross-references: EMBL:L37438; NID:9777717; PIDN:AABS9120.1; PID:9777718
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.4%; Score 86; DB 2; Length 347; Best Local Similarity 51.1%; Pred. No. 0.33; Matches 24; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.9%; Score 85; DB 2; Length 182; 61.4%; Pred. No. 0.25; tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406, 959-964, 2000
```

# GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 10.2532 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

US-09-816-989A-2 213 1 AKKYAKKAKAEKAKKAYKAA.....AKYEKAAAEKAAAKEAAYEA 45

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P06144 lytechinus	P19934 escherichia	Q08696 drosophila	Q9zhc5 mycobacteri	P15869 strongyloce	_	P29720 treponema p	Q11142 mycobacteri	_		-		_					Q07134 chironomus	P40278 chironomus	P40266 glyptotendi		•	-						Q08865 volvox cart	Q9rq15 bacteroides		P15864 mus musculu	Q93mh6 enterobacte
SUMMARIES	ID	H1 LYTPI	TOLA ECOLI	MST2_DROHY	DBH MYCSM	H1B_STRPU	DBH_MYCTU	TMPB TREPH	HBHA MYCTU	MST1_DROHY	TOLA PSEAE	DBH_MYCBO	H1_PARAN	HIE CHIPA	TOP1 STRCO	H1_SALTR	H1_ONCMY	H1G_STRPU	H10_CHITH	H1E CHITE	H11_GLYSA	H1_LYCES	RL22 DROME	H110_CHICK	H15_HUMAN	ASR_KLEPN	H12_GLYBA	H11_GLYBA	H1_WHEAT	H12_VOLCA	RS16 BACTN			ASR_ENTCL
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	Query Match Length	210	421	1391	208	211	214	384	198	344	347	205	248	235	952	194	206	217	244	237	233	287	299	219	225	139	232	233	238	240	184	212	211	101
de	Query Match	48.6	46.0	42.3	42.0	42.0	42.0	40.6	40.4	40.4	40.4	40.1	38.5	38.0	7		37.6	37.3	37.1		•	ġ.	ė.	ġ.	ė.	ů.	•	'n	'n	'n.	35.4	35.4	35.2	35.0
	Score	103.5	98	90	σ	89.5	σ	9	98	98	98	85.5	82	81	80.5	80	m	79.5	7	78.5	78	78	77.5	77	77	76.5	76.5	76.5	76.5		n	75.5	~	74.5
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P58122 caulobacter P39730 saccharomyc	P15276 pseudomonas P50565 chlamydomon P15796 caenorhabdi	P10771 caenorhabdi P43277 mus musculu P09426 anas platyr	P44678 haemophilus Q23858 dictyosteli	D08288 gallus gall
RS16_CAUCR IF2P_YEAST	ALGP_PSEAE H2B1_CHLRE H12_CAEEL	H11_CAEEL H13_MOUSE H1_ANAPL	TOLA HAEIN CRTC_DICDI	DBAZ SIRCO H11R_CHICK
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165 1002	352 153 190	207 220 217	372	218
35.0	34.7 34.3 34.3	34.3 34.3	34.0	33.0
74.5	74 73	73 73 72.5	72.5	7.5
3.4 3.5	36 37 38	3 4 4 4 0 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 4 4 2	* 4 * 3

# ALIGNMENTS

RESULT 1

H	10777
1	HILYTRI STANDARD: PRT: 210 AA.
AC	•
DI	988 (Rel.
DT	(Rel.
DŢ	. 38, Last
DE	Late histone H1.
SO:	Lytechinus pictus (Painted sea urchin).
ပ	Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
ပ္ပ	Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
ဗ	Lytechinus.
ŏ	NCBI TaxID=7653;
RN	_ [1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE=87040778; PubMed=3022245;
RA	Knowles J.A., Childs G.J.;
RT	"Comparison of the late H1 histone genes of the sea urchins
RT	Lytechinus pictus and Strongelocentrotus purpuratus.";
RL	
ប្ដ	-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
ပ္ပ	NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
ပ္ပ	
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S	•
נ	This SWISS-DBOT entry is convridit It is produced through a collaboration
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36	Detween the swiss institute of Bioinformatics and the Embi outstation
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ຍ	use by non-profit institutions as long as its content is in no way
ပ္ပ	modified and this statement is not removed. Usage by and for commercial
ບ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
ပ္ပ	or send an email to license@isb-sib.ch).
ນ	
DR	EMBL; X04488; CAA28177.1;
DR	PIR; A25550; A25550.
DR	HSSP; P02259; 1HST.
DR	InterPro; IPR001386; Histone H1/H5.
DR	InterPro; IPR003216; Linkerhist N.
DR	Pfam; PF00538; linker histone; 1.
DR	ProDom; PD000373; Linkerhist N; 1.
DR	SMART; SM00526; H15; 1.
X	Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
Š	10 AA; 2
ć	
5 6	48.05;
ที่ :	cal Similaricy es.14; Fred: NO. U.OULE;
Ma	Matches 28; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

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1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAABEKAAAKEAA 42 ||| ||| || || || || || || || || || || 1 166 AKKAAKKPAAKKPAAKKAAKPAKKAARKAAKKPAAKKAA 208 셤

RESULT 2 TOLA\_ECOLI

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                              Levengood S.K., Webster R.E.; "Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in Becherichia coli."; J. Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.

MEDLINE=99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plucckthun A., Wlodawer A.;
Lubkowski J., Hennecke F., Plucckthun A., Wlodawer A.;
Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA.";
Structure 7:711-722(1999).
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OP BACTERIOPHAGE DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97133271; PubMed-8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91296736; PubMed=2068069; Levengood S.K., Beyer W.F. Jr., Webster R.E.; Tolar a membrane protein involved in colicin uptake contains an extended helical region."; Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 421 AA
                                                                                     TolA protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
Escherichia coli.
                                                                                                                                                                                                                                             MEDLINE=90078104; PubMed=2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH PORINS.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                            NCBI_TaxID=562;
                                  01-FEB-1991
01-FEB-1991
                                                                                                                                                          Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       loubes R.;
 TOLA ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAINS
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SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE AND LAMB.
-!- SCHCELLULAR LOCATION: Type II membrane protein. Inner membrane.

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-- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
--- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Marzoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Eukaryota; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
EMBL; M28232; AAA24683.1; -.
EMBL, AE00017; AAC73833.1; -.
EMBL, D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
PDB; JTOL; 20.MAX-99.
ECGGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95045538; PubMed=7957199;
Neceson J., Padmanabhan S., Buenemann H.;
Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dhmst101 form extended
alpha-helical rods within the extremely elongated spermatozoa of
Drosophila hydel.",
Bur. J. Blochem. 225:1089-1095(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
-!- SUBCELLULIAR LOCATION: CYtoplaemic.
-!- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                               DOMAIN III (FUNCTIONAL)
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                                                                                                                                    46.0%; Score 98; DB 1; Length 421; 65.3%; Pred. No. 0.0097; tive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 KKAABEKAAABEKAAADKKAAABKAAABKAAAA-AKAAABKAAAAKAAABA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Inner membrane; 3D-structure; Complete proteome.
DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                         PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
                                                                                                                                                                                                                                                                                                           8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1391 AA
                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Axoneme-associated protein mst101(2).
                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 65.3
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                    13
34
421
310
421
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7224;
                                                                                                                                                                                          14
35
48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEATS.
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                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MST101(2)
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MST2 DROHY
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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211 AA.

STANDARD;

us-09-816-989a-2.open.rsp

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or send an email to license@isb-sib.ch)
                                                       EMBL; X73481; CAA51876.1; -.
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SSEREFFS

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Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                     MEDINE 88246461; PubMed=2837660;
Lai Z.-C., Childs G.;
Lai Z.-C., Childs G.;
"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urchin Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988)
-:- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-:- SUBCELLULAR LOCATION: Nuclear.
-:- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                             01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone Hi-beta, late embryonic.
                                                 01-APR-1990 (Rel. 14, Created)
                                                                                                                                       Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                             SEQUENCE FROM N.A.
                         HIB STRPU P15869;
RESULT 5
HIB_STRPU
                                     ä
         PIR; S34154; S34154.
FlyBase; FBGn0020733; Dhyd\mst101(2).
Sperm; Repeat; Multigene family; Polymorphism.
DOMAIN 332 1268 59 X 16 AA APPROXIMATE TANDEM REPEATS OF [KR] -K-X-C-X-X-X-X-X-X-X-E.
SEQUENCE 1391 AA; 159000 MW; 1B2A368F30F48878 CRC64;
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STAINA-ATCC 700084 / mc(2)155;
MEDLINE=99110.209; PubMed=9894918;
Lee B.H., Murugasu.Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                   DB 1; Length 1391;
                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
LacCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last senotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
                                                                                                                           11; Indels
                                                                                                                                                                   663 KETAEKKKCEKAAKKRKEAAEKKKCABAAKKEKEBAAEKKKCEBAA 707
                                                                                                                                                   42.3%; Score 90; DB 1; 57.8%; Pred. No. 0.15; iive 4; Mismatches
                                                                                                                                                                                                                                            208 AA.
                                                                                                              Local Similarity 57.8
les 26; Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                  Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1772;
                                                                                                                                                                                                                                                      Q9ZHC5;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                     OR HLP
                                                                                                                                                                                                                                           DBH MYCSM
                                                                                                   Query Match
                                                                                                                                                                                                                            Matches
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InterPro; IPR001386; Histone H1/H5.
InterPro; IPR001316; Linkerhist N.
Pram, PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
SMART; SM00526; H15; I. EMBL; M20314; AAA30052.1; -. PIR; A28100; A28100.

Query Match
42.0%; Score 89.5; DB 1; Length 2
Best Local Similarity 61.9%; Pred. No. 0.034;
Matches 26; Conservative 3; Mismatches 10; Indels 139 SKKTTKKVKKPAAKKAKPA-AKKAAK--KPAAKKPAAKKAA 177 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42 셤 ઠ

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send an email to license@isb-sib.ch).

EMBL; AF068138; AAD13809.1.; -. HSSP; P02346; 1HUU.

1. Gen. Genet. 260:475-479(1998).
PUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOUTC UNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.

smegmatis."

2;

Gaps

ë.

DB 1; Length 211;

STANDARD; DBH\_MYCTU P95109; RESULT 6 DBH MYCTU

15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 40, Last annotation update)
16-JUL-1999 (Rel. 40, Last annotation update)
18-JUL-1999 (Rel. 40, Last annotation update)
18-JUL-1999 (Rel. 40, Last annotation update)
18-JUL-1999 (Rel. 40, Last sequence update)
18-JUL-1999 (Rel. 40, Last sequence update)
18-JUL-1999 (Rel. 40, Last sequence update)
19-JUL-1999 (Rel. 40, Last 

Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium. NCBI\_TaxID=1773; Mycobacterium tuberculosis.

SEQUENCE FROM N.A. STRAIN=H37Rv;

;

Gaps

9 45

13; Indels

3; Mismatches 42.0%; Score 89.5; 53.7%; Pred. No. 0.

Conservative

Similarity

Local Sim

Matches

셤

Query Match

DB 1; Length 208;

0.033;

DEGENERATE REPEATS REGION.
CASF577F61F7EF09 CRC64;

21230 MW;

208 AA;

SEQUENCE

DNA-binding; DNA condensation; Repeat.

InterPro, IPR000119; Bac\_DNAbind.
Pfam; PF00216; Bac\_DNA\_binding; 1.
ProDom; PD000945; Bac\_DNAbind; 1.
SMART; SM00411; BHL; 1. PROSITE; PS00045; HISTONE LIKE; 1 

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                                                                                                                                                                                                                                                                  Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Slivtensky L., Schouls L.M., van Embden J.D., Charon N.W.; Slivtensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991).
-!- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR LARGE MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
[ED].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA TANDEM REPEATS OF [EA] - A-A-R-X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.6%; Score 86.5; DB 1; Length 384;
      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6E94CBC74294DE8C CRC64;
                                                                                                       Treponema phagedenis.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
Noil_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.11;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-17.
6 X 8 .
A-A-E.
                                                                                                                                                                                                                            STRAIN=Kazan 5;
MEDLINE=91372983; PubMed=1894368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M58563; AAA27480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
245
254
263
272
281
384 AA;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alband D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                 Harris D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglineier K., Gas S., Barry C.E. III, Tekaia F., Backock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares R., Seeger K., Skelton S., Squares S., Squares R., Torlor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Savita P.;
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
PROKARYOTIC DNA-BINDING PROTEINS TIS DENATURATION UNDER EXTREME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%; Score 89.5; DB 1; Length 214; 55.6%; Pred. No. 0.034; Live 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMIS; PRO0216; Bac DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
PRINTS; PR00624; HISTONEHS.
PRODOM; PR000945; Bac DNAbind; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
DNA-binding; DNA condensation; Repart; Complete proteome.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.
DOMAIN 101 214 DEGENERALE REPEATS RECION.
SEQUENCE 214 AA; 22187 MW; CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculist; Rv2986c; -.
InterPro; IPR000119; Bac_DNAbind.
InterPro; IPR001386; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z83018; CAB05427.1; -.
EMBL; AE007127; AAK47393.1; -.
HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; MT3064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
TMPB_TREPH
ID TMPB_TREPH
AC P29720;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
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Gaps
 1;
13; Indels
                                    1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
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384 AA

STANDARD;

Matches

8

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Nature 412:190-194 (2001).
-!- FUNCTION: REQUIRED FOR EXTRAPULMONARY DISSEMINATION. MEDIATES
ADHERENCE TO EPITHELIAL CELLS BY BINDING TO SULFATED
GLYCOCONJUGATES PRESENT AT THE SURRACE OF THESE CELLS; BINDS
HEPARIN, DEXTRAN SULFATE, FUCCIDAN AND CHONDROITIN SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=M tuberculosis; STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haff D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                 SPECISES-M. tuberculosis; STRAIN=H37Rv;
MEDLINE=9825987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Rothwell T., Gentles S., Hamiln N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Geborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteria (class), Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                               SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
SPECIES-Mutuberculosis, and M.bovis;
STRAIN-H37RV, ATCC 201 / H37Ra, and BCG / Paris 1173 P2;
MEDLINE-98445421; Pubmed-9770536;
Menozzi P.D., Bischoff R., Fort E., Brennan M.J., Locht C.;
Menozzi P.D., ansotorization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin.";
Proc. Natl. Acad. Sci. U.S.A. 95:12625-12630(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=103, and BCG;
MEDILIBE=21342355; PubMed=11449276;
Pethe K., Alonso S., Biet F., Delogu G., Brennan M.J., Locht C.,
Menozzi F.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M., Muller J., Bischoff R., Brennan M.J., Locht C., Indentification of a heparin-binding hemagglutinin present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNCE OF 1-16, AND CHARACTERIZATION.
SPECIES=M.tuberculosis, and M.bovis;
STRAIN=ATCC 201 / H37Ra, and BCG / Paris 1173 P2;
MEDLINE=97188915; PubMed=9064359;
                                             011142; 085733;
01-0CT-1996 (Rel. 34, Created)
10-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Heparin-binding hemagglutinin (Adhesin).
Mycobacterium tuberculosis, and
                                 198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=M.tuberculosis, and M.bovis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exp. Med. 184:993-1001(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:537-544(1998).
                               STANDARD;
                                                                                                                                                                    Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION.
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                                                                                                                                                                                                                                                                 MISCELLANEOUS: SERUM FROM PATIENTS DIAGNOSED WITH ACTIVE TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES THAT RECOGNIZE HBHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITRE=94200512; PubMed=8150205;
Messen J., Buenemann H., Heinlein U.A.;
Neesen J., Buenemann H., Heinlein U.A.;
Neesen J., Buenemann H., Heinlein U.A.;
Neesen J., Suenemann H., Heinlein U.A.;
Neesen J., Buenemann H., Heinlein U.A.;
repetitive, axoneme-associated protein with differential abundance in Y chromosomal deletion mutant files.";
Dev. Biol. 162-1414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTUREL ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SPERMATID BUNDLES.
PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Ilnsecta; Pterygota; Neoplera; Bndopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                    DOMAIN OF HEALT PROTEINS TRUNCATIONS FROM THE C-TERMINAL END DIMINISH THE AFFINITY FOR HEPARIN.

DIMINISH THE AFFINITY FOR HEPARIN.

PTM: GLYCOSYLATED. GLYCOSYLATION MAY PROTECT THE PROTEIN FROM PROTECLYTIC DEGRADATION AND BE IMPORTANT FOR HEMAGGLUTINATION. I'S UGGESTS THAT THE CARBOHYDRATE MOIETY MAY BE LOCATED WITHIN THE TERMINAL DOMAIN OF HBHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z77162; CAB00936.1; -.
EMBL; AE06951; AAK44716.1; ALT_INIT.
TIGR; MT0493; -.
Tuberculist; Rv0475; -.
Cell adhesion; Heparin-binding; Hemagglutinin; Glycoprotein; Virtlence; Complete proteome.
                         INDUCES MYCOBACTERIAL AGGRECATION.
SUBCELLULAR LOCATION: SURFACE ASSOCIATED.
DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.4%; Score 86; DB 1; Length 198; ilarity 65.6%; Pred. No. 0.068; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 193 ALA/LYS-RICH.
120 120 R -> P (IN REF. 1).
198 AA; 21403 MW; 513760F6FIEB6042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: STRONG, TO M.LEPRAE HBHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF074390; AAC26052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MST1_DROHY
Q08695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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European Bioinformatics Institute.
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                                                                                                                                                                                         TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
     STITIES
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Bordy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                        19 X 16 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                       K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X. 344 AA; 37793 MW; 24C65D2510387E2A CRC64;
   -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELLCAL.
-!- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    귱
                                                                                                                                                                                                                                                                                                                        Query Match
40.4%; Score 86; DB 1; Length 344;
Best Local Similarity 57.8%; Pred. No. 0.11;
Matches 26; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dennis J.J., Lafontaine B.R., Sokol P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            117 KEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 161
                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 AA
                                                                                                                                                                                    EMBL; X73480; CAA51875.1; -.
PIR; S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                             Sperm; Repeat; Multigene family.

DOMAIN 58 337 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:959-964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tola protein.
TOLA OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSEAE
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                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                     EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BCG / Tokyo;
Mateumoto S., Yukitake H., Mateuo T., Mineda T., Yamada T.;
Mateumoto S., Yukitake H., Mateuo T., Mineda T., Yamada T.;
Identification of a novel protein generating bacterial slow growth
From Mycobacterium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBH MYCBO STANDARD; PRT; 205 AA.
Q9XB18, Q9S5J5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
BNA-binding protein HU homolog (Histone-like protein) (Hlp)
                                                                                                                                                                                                                                                                                                                                                                         40.4%; Score 86; DB 1; Length 347; llarity 51.1%; Pred. No. 0.11; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AOKAAEAKKADEAKKAAEAKAAEOKKOADIAKKRAEDEAKKKAAEDA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                        209 216 POLY-ALA.
347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                            POTENTIAL. PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB013441; BAA78330.1; -.
HSSP; P02346; 1HUU.
ILLEPPO; IPR000119; Bac DNAbind.
INTERPO; IPR001386; Histone_H1/H5.
Pfam; PP00216; Bac_DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
PRODOM; PD0000945; Bac_DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y18421; CAB46493.1; -.
                                                                                                                                                             EMBL; AE004530; AAG04360.1;
                                                                                                                                          EMBL; U39558; AAC44660.2;
                                                                                                                                                                                                                                      16
37
347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 24; Conserv
                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=1902;
                                                                                                                                  01-FEB-1995 (
01-FEB-1995 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 KKA 188
                                                                                                                                                                                                        Histone H1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 YEA 45
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                                                                                           CHIPA
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Q9X909,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of histone H1 from sperm of the sea urchin
Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the
protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the entire primary structure.";

Eur. J. Blochem. 104:567-578(1980).
-!- RUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- STRUCTURES.
-!- SPECIALITY: SPERM.
-!- SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
                                                                                                                                                                                                                                ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                 90 BACTERIAL HISTONE-LIKE DOMAIN.
205 DEGENERATE REPEATS REGION.
199 A -> T (IN REF. 2).
21262 MW; 19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parechinus angulosus (Angulate sea urchin).
Eukaryota, Metazoa, Echinodermata, Bleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Echinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 248;
                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                                                                                                   DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 144 K -> R.
248 AA; 26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 KKAKKTSAAAKAKA-KAAAKKARKAKAAAKKKAALAKKKAAAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAA-AKEAAYEA 45
                                                                                                                                                                                                                                                                                                    111 AKKVAKKAPAKKATKAAKKAATKAPA---KKAATKAPAKKA 148
                                                                                                                                                                                                                                                                     1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
                                                                                                                                                                               40.1%; Score 85.5; DB 1
58.5%; Pred. No. 0.078;
iive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.5%; Score 82; DB 1
57.8%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
SMART; SM00411; BHL; 1.
PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001386; Histone HI/HS.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00526; H15; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02586; HSURIP.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histone H1, gonadal.
                                                                                      101
199
105 AA;
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 80-248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE OF 1-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parechinus
                                                                                                             CONFLICT
                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                             H1_PARAN
P02256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                      DOMAIN
                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
HIPARAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Petrygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomodea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 235 AA; 24446 MW; 340BC5B9A85002AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA topoisomerase I EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
(Untwisting enzyme) (Swivelsee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                      Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach U. Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%; Score 81; DB 1; Length 235; llarity 41.3%; Pred. No. 0.23; Conservative 2; Mismatches 17; Indels
                                                                                   (Rel. 31, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          952 AA.
235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR003216; Linkerhist. N.
Pfam; PP00538; linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
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MEDLINE=21996410; PubMed=12000953;
                                                     (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L29106; AAA21714.1; -. HSSP; P08287; 1GHC.
STANDARD;
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es 26; Conserv
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=7151;
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MEDLINE=78023898; PubMed=913397;

MEDLINE=78023898; PubMed=913397;

MCLEOD A.R., Wong N.C.W., Dixon G.H.;

MCLEOD A.R., Wong N.C.W., Dixon G.H.;

Eur. J. Blochem. 78.281-291(1977).

-1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEDSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-1- SUBCELLULAR LOCATION: NUClear.

-1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.

RR PR., A05283; H97R1.

RRSSP, P08287; 1GHC.

InterPro; IPR001386; Histone H1/H5.

RRSSP, P080538; Linker histone; 1.

R Promo, P0000373; Linkerhist_N; 1.

R MART; SMO526; H15; Inkerhist_N; 1.

R MART; SMO526; H15; Inkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AA; 19408 MW;
                                                                                                                                                                                                                                                                                                                                                  Acetylation; Phosphorylation. MOD RES 1
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161
182
100
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SEQUENCE
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MOD_RES
MOD_RES
DOMAIN
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        SEOUENCE
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              OCCITION TA (2). ".

Nature 417:41-147(2002).

- 1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLGGICAL ISOMER OF DNA TO ANOTHER.
- 1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
- 1- SUBUNIT: MONOMER (BY SIMILARITY).
- 1- MISCELLANBOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYNGSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME IS JOINED TO A DNA PHOSPHORUS IS JUILARITY: BELONGS TO PROKARYCTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Golle A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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InterPro: IRR003601; DNAtopi_ATP bind.

InterPro: IRR003601; DNAtopi_DNA_bind.

InterPro: IRR003801; Prox tpisomrase.

R InterPro: IRR003801; Prox tpisomrase.

R Fam; PF01131; Topoisom bac; 1.

R Fam; PF01131; Topoisom bac; 1.

R RANT; SM00437; TOPIAc; 1.

R SMART; SM00436; TOPIBc; 1.

R SMART; SM00436; TOPIBc; 1.

R SMART; SM00436; TOPIBc; 1.

R TIGRFAM; TGR0151; topA bact; 1.

R TIGRFAM; TGR0151; topA bact; 1.

R TIGRFAM; TGR0151; topA bact; 1.

R TIGRFAM; TGR0153; TOPISOMERASE I PRCK; 1.

R ROSITE; PS00396; TOPOISOMERASE I PRCK; 1.

R ACT SITE 334 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 952 AA; 103584 MW; 1C98DABD7A629295 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%; Score 80.5; DB 1; Length 952; 55.6%; Pred. No. 0.86; tive 2; Mismatches 15; Indels
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les 25; Conservative
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Salmo trutta (Brown trout).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Neoplerygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

15-JUL-1999 (Rel. 38, Last annotation update) Histone H1.

RESULT 15
H1 SALTR
10 P1 225
AC P0225
DT 21-JU
DT 21-JU
DT 15-JU
DE Histo
OS Salmo
OC Actin
OC Prota

21-JUL-1986 (Rel. 01, Created)

STANDARD;

H1\_SALTR P02254;

888 AKKTAKKAVKKTAAKKAPAKKAAATKKTAAAKTTAAKKTAAKSTA 932

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2
                                                                          Gaps
                                                                          4.
                                           Score 80; DB 1; Length 194; Pred. No. 0.25;
1 -> I (IN MINOR COMPONENT).
D288F9F44AF9BE7E CRC64;
                                                                         13; Indels
                                                                                                                       105 AKKPAKKAAAPKAKKVAAKKPAAAKKPKKVAAKKAVAAKKSPKKA 149
                                                                                                      41
                                                                                                      37.6%; Scor.
55.6%; Pred. No. u.....
.... 3; Mismatches
                                                                                                                                                                            Search completed: March 10, 2003, 12:17:08 Job time: 11.2532 secs
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ACETYLATION (IN 90% OF THE CHAINS).

PHOSPHORYLATION. PHOSPHORYLATION. GLOBULAR. PHOSPHORYLATION

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 , Search time 23.8291 Seconds (without alignments) 389.109 Million cell updates/sec Run on:

US-09-816-989A-2 213 Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

SPTREMBL 21:\* Database

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\* sp\_organelle:\* sp\_phage:\* sp\_mhc: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp\_bacteriap:\* sp archeap:\* rvirus:\* 111: 12: 13: 14: 15:

sp\_unclassified:\* sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*

sp\_plant:\*

S	Dooring		Q8x965 escherichia	Q8y5w4 listeria mo	Q9ajx2 streptomyce	Q92a67 listeria in	O01395 drosophila	Q9wwx1 pseudomonas	Q9a5j6 caulobacter	Q8xvn7 ralstonia s	093946 candida alb	Q8wq44 leishmania	Q9bmy8 leishmania	Q8t9r3 leishmania	Q45370 bordetella	Q9u3w3 caenorhabdi	Q8qndl ectocarpus	Q9at18 lens culina
SUMMARIES	Ę		Q8X965	Q8Y5W4	Q9AJX2	Q92A67	001395	Q9WWX1	Q9A5J6	Q8XVN7	093946	Q8WQ44	Q9BMY8	Q8T9R3	Q45370	Q9U3W3	Q8QND1	Q9AT18
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	& Query Match	יומירי	46.0	44.4	42.7	42.3	41.5	41.5	41.3	40.6	40.4	39.9	39.9	39.9	39.9	39.4	39.2	39.0
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	Result		7	7	e	4	S	9	7	89	0	10	11	12	13	14	15	16

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6 Q9CM70 Q23784 6 Q9S2M2 O94567	Q93LK4 Q9NFP6 Q9XYY5 Q23790	•		0000	0 0
389 243 262 568 31	4 8 8 2 2 2 4 1 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2		297 10 301 10 306 10 277 16		291 16 293 10 347 16 969 5 1340 16 407 16
39.0 38.5 38.5 4		38.000	38.0 38.0 37.8	37.8 37.6 37.6 37.6	37.6 37.6 37.6 37.6 37.6 37.3
83 82.5 82 82 82	81.5 81.5 81 81	881 81 81 81	81 81 81 80.5	80.5 80 80 80 80	80 80 80 80 79.5
118 118 20 20	1 0 0 0 0 1 0 0 4 0	2 2 2 2 3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	33 33 33 33 33 33 33 33 33 33 33 34 34 3	8 8 8 8 8 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8	W 4 4 4 4 4 4 0 0 0 11 12 12 12 12 12 12 12 12 12 12 12 12

# ALIGNMENTS

SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0508952;
STRAIN=0157:H7 / RIMD 0508952;
STRAIN=0157:H7 / RIMD 0508952;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Secherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res 8.11-22(2001).
EMBL; AR005252; AAGS6075.1; -. STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

Rosen D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potemousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TOLA OR 20907 OR ECS0774.
BScherichia coli 0157:H7. Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae, 394 AA. PRT; Nature 409:529-533(2001). PRELIMINARY; NCBI\_TaxID=83334; SEQUENCE FROM N.A. Escherichia. 

Taylor K.

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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                Hopwood D.A.;
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Matches
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7
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser P., Frangel L., Buchrieser C., Rusniok C., Amend A., Charabott P., Charabotty T., Charabit A., Checouni F., Couve E., de Daruvar A., Dehoux P., Domann E., Domiguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez W., Hain T., Hauf J., Jackson D., Jones L. M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Raquez-Boland J.-A., Voss H., Wehland J., Cossart P., (Comparative genomics of Listeria species.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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Pred. No. 0.053;
7; Mismatches 9; Indels 5;
                                                                                                                                                 Score 98; DB 16; Length 394;
Pred. No. 0.04;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                            220 KKAAEKAAAEKAAADKKAAAEKAADKKAAA-AKAAAEKAAAAKAAAEA 267
                                                                                                                                                                                                                                                                                  Complete proteome.
5836 MW; 72E59D576E0D7832 CRC64;
                                                                                          394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
Complete proteome.
SEQUENCE 394 AA; 40517 MW; SB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:849-852(2001).
EMBL, AL591981; CAD00019.1; -.
Listilist; LM001941; -.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete pi
                                                                                                                                                       46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein 1mo1941
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STRAIN=EGD-E / SEROVAR 1/2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                              Query Match
Best Local Similarity 65.3%
....hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative secreted protein. SCO1805 OR SCI33.04. Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8Y5W4
Q8Y5W4;
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(089584
100 89458
100 89458
101-M
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ID Q9
DJ Q0
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Checuani F., Couve E., de Daruvar A., Dehoux P.,
Bentian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Gebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maltournam A., Mata Vicente J., NG E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AKKAAEEKAAAEKAAEEKKAAEEKAAADKKSQEDEAAKAAAAKKEQEAAEEKAAAEKAAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Gaps
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Auture 417:141-147(2002).
EMBL; AL513407; CAC26545.1; -.
SEQUENCE 244 AA; 25524 MW; 61999D62CA23A7B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 91; DB 16; Length 244; 59.5%; Pred. No. 0.12; ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.3%; Score 90; DB 16; Length 243; 45.5%; Pred. No. 0.15; ive 3; Mismatches 11; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ll procein; Complete proteome.
243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 SOKVAAIBAKKEAAAKKATAKKATAEKKAAAEKAAAKRAAKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin2055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AKKAKAEKAKK--AYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ALS96170; CAC97285.1; -. ListList; LIN02055; -. InterPro; TPR002482; LysM. Pfam; PF01476; LysM; 1. Hypothetical protein; Complete in the complete in the
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 59.5'
Matches 25; Conservative
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hes 30; Conserv
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STRAIN-ATCC 1908) / CB15;

MEDLINE-21173698; PubMed=11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Bly B., Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonnay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Wamathevan J., Ermolaeva M., White O. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Proc. Natl. Acad. SGI. U.S.A. 98:4136-4141(2011).

Proc. Natl. Acad. SGI. U.S.A. 98:41320 BY TOPOISONERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY
                                                                                                                                                                                                                                    Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5835-5846(1996).
EMBL; X74218; CAB50780.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.5%; Score 88.5; DB 2; Length 372; 39.7%; Pred. No. 0.31; ive 8; Mismatches 10; Indels 23
                                                          Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DNA topoisomerase (EC 5.99.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAA----
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TIGR; CC2451; -.
InterPro; IPR002936; DNAprim_toprim.
InterPro; IPR003601; DNAtopl ATP bind.
InterPro; IPR003602; DNAtopl_DNA_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000380; Prok tpisomrase.
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                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001386; Histone H1/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 372 AA; 40133 MW; 87F4
                                                                                                                                                                                                           MEDLINE=96422022; PubMed=8824639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE005914; AAK24422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 39.7 tes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=155892;
   FROM N.A.
                                                                                                                                                SEQUENCE FROM N.A.
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181 AEEAKKKA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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      셤
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                                                                                                                                                                                                                                                                                                                                                                                           Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 X 16 AA APPROXIMATE TANDEM REPEATS OF X-[KQ]]-K-C-[AE]-E-X-A-[X]-K-X-X-X-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of the
cell envelope.";
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Nessen J., Heinlein U.A.O., Buenemann H.,
Submitted (JAN.1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88.5; DB 5; Length 275; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1-SUBCELLULARITY.
-1-TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-1-DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
BRML; U85627; AAB51369.1; -.
Flybase; FBGN020732; Dhyd\mst101(3).
Sperm; Repeat; Multigene family.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
101-JURA-2001 (TrEMBLrel. 16, Last annotation update)
Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 178:1699-1706(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 AA; 30436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.5%;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.0
                                                                                                                                                                                                           PRELIMINARY;
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                                 NCBI_TaxID=303;
39 KEAAYE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tola protein.
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RESULT 6

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Matches

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SEQUENCE FROM N.A.
Kaiser B., Kunkel W., Saluz H.P., Munder T.;
"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

BENBL; AJ006637; CAA07165.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K.P., "Identification and characterization of a novel Leishmania gene encoding for a putative histone H1- like transcription factor.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                              Query Match 40.4%; Score 86; DB 3; Length 212; Best Local Similarity 48.9%; Pred. No. 0.31; Matches 23; Conservative 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melo G.S., Fragoso S.P., Fasel N.S., Mendonca S.C.F., a "Cloning and sequencing of histone H1 gene from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%; Score 85; DB 5; Length 98; larity 55.0%; Pred. No. 0.19; Conservative 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                     Submitted (UL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP227632; AAG60608.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                        SEQUENCE 212 AA; 24231 MW; 10C2122E9554A387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA; 9999 MW; 0A4AB93089D6C261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania amazonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 kDa nuclear protein
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                     NCBI_TaxID=5476;
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Q9BMY8;
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Q8WQ44
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Matches
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  STREETERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arliguenave Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "InterPro; IPR000104; Antifreeze_1.
                                                                                                                                                                                                                                                                                     5,
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Pred. No. 0.27;
4; Mismatches 11; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                           / Match 41.3%; Score 88; DB 16; Length 899; Local Similarity 58.7%; Pred. No. 0.82; nes 27; Conservative 5; Mismatches 12; Indels
                                                                                                                                    TIGREAMS; TIGRO1051; topA bact; 1.
PROSITE; PS00396; TOPOISOMERASE I PROK; 1.
DNA-binding; Isomerase; Topoisomerase; Complete proteome.
SEQUENCE 899 AA; 97723 MW; 1485DC4EDA0DA6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAKAEKAK-KAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21681879; PubMed=11823852;
              Pfam; PF01751; Toprim; I.
Pfam; PF0136; zf-C4 Topoisom; 1.
PRINTS; PR00417; PRTPISMTASEI.
SMART; SM00437; TOP1Ac; 1.
SMART; SM00436; TOP1Bc; 1.
SMART; SM00493; TOPRIM; 1.
Topoisom_bac; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable histone H1 protein. RSC2793 OR RS00453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00308; ANTIFREEZEI
PRINTS; PR01503; TREACLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, CTA2p (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTA2. Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 56.5
tes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE 200 AA;
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Pfam; PF01131;
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Best Loca Matches

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RESULT 9
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DT 01-N9
DE 01-N9
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OS CAA2

Q8XVN7

RESULT 8

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101 AA; 10078 MW; 3D3AE865FD9B6846 CRC64;

SEQUENCE

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF216291; AAF23175.1; -.
EMBL; US8757; AAK66021.1; -.
                                                                                                                                                                                                                                    Jedrusik M.A., Schulze E.; "The histone H1 complement of Caenorhabditis elegans."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid C01B10.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Histone H1.Q (Hypothetical 6.2 kDa protein)
                                  60 AA.
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                                                                Created)
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                                  PRT;
                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 58.1%;
Matches 25; Conservative
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
ESV-1-151.
                                                            01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00624; HISTONEHS
                                  PRELIMINARY;
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                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome.";
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 RESULT 14
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Papageorgiou F., Soteriadou K.;
"Identification of a Leishmania infantum gene encoding for an histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarlato V., Arico B., Goyard S., Ricci S., Manetti R., Prugnola A., Manetti R., Polverino-De-Laureto P., Ullmann A., Rappuoli R.;
"A novel chromatin-forming histone H1 homologue is encoded by a dispensable and growth-regulated gene in Bordetella pertussis.";
EMBL, L37438; AAB59120.1;
SEQUENCE 182 AA; 18252 MW; 9A17A397B12B0421 CRC64;
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                  Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania
NCBI_TaxID=5671;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.9%; Score 85; DB 5; Length 111; 55.0%; Pred. No. 0.21; tive 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 85; DB 2; Length 182; Pred. No. 0.34;
                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                H1-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469106; AAL76335.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AA; 11162 MW; 16168F3B54960E83 CRC64;
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 AKKPAKKVAKKPAKKPAKKPAKKAAKKAAKKAAAKK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKE 40
39.9%; Score 85; DB 5; 60.0%; Pred. No. 0.19; cive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AA.
                                                                                                                                                                           111 AA
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                                                                                                                                                                                                        Created)
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                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95319329; PubMed=7596289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08,
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61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guery Match
Best Local Similarity 55.0°
Matches 22; Conservative
                               27; Conservative
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                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                   18 kDa nuclear protein.
Leishmania infantum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein.
SEQUENCE 111 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BPW28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
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Query Match
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                               Matches
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2,
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                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
                                                                                                                                     5
                                                                            Score 84; DB 5; Length 60; Pred. No. 0.14;
                                                                                                                                     Indels
Hypothetical protein.
SEQUENCE 60 AA; 6212 MW; D01ABB4CEC35566D CRC64;
                                                                                                                                                                                       2 KKYAKKAKAEKAKKAY-KAAEAKKAAK-YEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                          14 KKVAAKPKAPKVKKASPKKAAAPKAKKPVKKAAAKKSPAKKAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                12;
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g

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1; Gaps
                                                                                        Query Match
Best Local Similarity 52.3%; Pred. No. 1.2;
Matches 23; Conservative 5; Mismatches 15; Indels 1;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF204951; AAK14566.1; -. SEQUENCE 483 AA; 53368 MW; F85241B7B6A6913B CRC64;
    SSR
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Search completed: March 10, 2003, 12:25:54 Job time : 25.8291 secs

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March 10, 2003, 12:15:01; Search time 23.4494 Seconds (without alignments) 255.712 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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213
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DB	, di	Description
	213	100.0	1	21.	AAY82572	Copolymer molecula
α	138	64.8	109	21	AAY82577	Copolymer molecula
m	134.5	63.1		21	AAY82573	Copolymer molecula
4	131	61.5	77	21	AAY82575	Copolymer molecula
Z)	126.5	59.4		21	AAY82576	Copolymer molecula
9	120.5	9.95		21	AAY82574	Copolymer molecula
7	108	50.7	35	21	AAY82571	Copolymer molecula
ω	99.5	46.7		17	AAR06446	Recombinant copoly
6	98	46.0	46	13	AAR28871	High affinity macr
10	94.5	44.4	•	23	ABB49123	Listeria monocytog

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

98US-0101693.

25-SEP-1998;

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	1:	5	7.57	100	40	ro	ū
	1 -	σ	42.0	214	2	20724055	1024
	7 5			214	3 5	かなななななる	tuberculosis
	י ר ל ר	•	4 C	756	4 0	CCCCCAR	rel human dian
	1 4	9	0	יי פרי	10	ANEAA024	Mycobacterial hena
	17	9 6	0	1 0 0	1 6	AAW43082	
	1 2	9 8		1 6 6 1	16	AAW44936	
	19	85.5		202	51	AAB20575	
	20	85	9	427	22	AAG70868	
	21	82	8	165	22	AAG91997	C glutamicum prote
•	22	77.5	ė.	299	22	ABB63276	Drosophila melanog
	23	77.5	ė.	2151	22	ABB60086	
	24	11	ė.	103	20	AAY34067	Histone H1 isoform
	25	77	ώ,	103	21	AAY57365	Human histone H1.5
	9 10	7.7	٠.	116	0 7	AAY34066	Histone HI isolorm
	27	7.7	36.2	116	77	AAY57364	Human histone Hi.5
	9 0			1 L	2 6	AA134068 aave7366	Himan histone H1 5
	30	77		222	18	AAW29476	histone H1
	31	77	. 6	222	20	AAY34033	histone
	32	77	9	222	21	AAY57331	histone H1
	33	77	9	226	20	AAY34060	histone H1
	34	77		226	21	AAY57358	Human histone H1 i
	35	9/	5	157	22	ABB58855	hila
	36	75.5	ď.	111	23	ABP00299	Human ORFX protein
	37	LO.	υ.	201	23	ABP41465	
	38	ഹ	ω.	218	21	AAG00755	secreted
	9.0	75.5	٠. د	218	7 7	AAG00759	secreted
	2 ·	Ωı	٠	220	57	AAU / 69 / 2	ribosoma
	14.	ΛI	٠	577	7.7	AAG00758	
	24.5	S.	٠. ن	265	7.	7	Lung cancer associ
	6.	•		160	B) (B	AAW14549	Streptococcus pneu
	44	4	35.0	32	9	8	Polycationic polyp
	45	74.5	υ.	32	18	AAW06686	Protamine-like pep
						CHARLACTE	
						ALIGNMENTS	
RESULT	JLT 1						
AAY	AAY82572						
13	AAY82	572	standard;	peptide		45 AA.	
Ž,							
¥ X	AA1825/2	17/07					
E S	28-JI	-JUL-2000	(first	t entry)	۶ ک		
<b>1</b> 8	Copo]	Copolymer m	molecular	r weight		TV-marker amino acid sequence	nce SEQ ID NO:2.
\$	Copo]	Copolymer;	molecula	ar wei	ghtr	molecular weight marker; TV-marker; immune disease;	disease;
1	3		3		1	ונו לדם נוספני מייר בייר נייר לו	10. 10. 10. 10. 10. 10. 10. 10. 10. 10.

glatiamer acetae; autonimmue otsease; antianthilo; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabenic; immunosuppressive; demyelinating disease; osteoarthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellituis; Graves disease; Guillain-Barre's syndrome; psoriasis; hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. 99WO-US22402 WO200018794-A1 Unidentified 24-SEP-1999; 06-APR-2000. 

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition orcresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for and an amino acid composition are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune barnels and insease, chronic immune thrombocytopaenia uveoretinitis, crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, psyndrome, Hashimoco's disease, alidopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, giraft-versus-serial disease, and delayed-type hypersenitivity. The polypeptides of the invention have defined molecular weights and physpetides of the invention have mylernian weights and physpetides them ideal for use as
                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                     Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular weight markers.
                                                                                   WPI; 2000-317499/27.
                               Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                               Gad A,
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune antibody-mediated diseases. Such diseases include arthritic conditions, antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anomemia, autoimmune opophoritis, osteoarthritis, autoimmune the among autoimmune buseness, diabetes mellitus, Graves disease, Guillain-Barre's sonfactiasis, pemphigus vulgaris, or systemic contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, psentiasis, pemphigus vulgaris, or systemic contact sensitivity diseases which can be treated contact sensitivity diseases which can be treated contact sensitivity diseases which can be treated contacts and contact sensitivity diseases which can be treated contacts and co

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Lis D;

Gad A,

98US-0101693.

25-SEP-1998;

Claim 10; Page 14; 72pp; English.

include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensityutty. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as

45 AA;

Gaps .; 0 45 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA Local Similarity 100. ses 45; Conservative Query Match Matches a ò

AAY82577 standard; peptide; 109 AA AAY82577; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

(first entry)

28-JUL-2000

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; hemostatic; antiporiatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. 

WO200018794-A1.

06-APR-2000

Unidentified

99WO-US22402. 24-SEP-1999;

ö 100.0%; Score 213; DB 21; Length 45; 100.0%; Pred. No. 1.4e-16; ive 0; Mismatches 0; Indels 

7

Gaps

4;

64.8%; Score 138; DB 21; Length 109; 76.6%; Pred. No. 5.1e-08; ive 0; Mismatches 7; Indels

Query Match
Best Local Similarity 76.6
Matches 36; Conservative

molecular weight markers

109 AA;

Sequence

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glatitamer acctate; autoimmune disease; antiathritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antidiabetic; thyrominetic; haemostatic; antipaoriatic; dermatorojoical; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gullain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                      Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                  Copolymer; molecular weight marker; TV-marker; immune disease;
                                         65 AKKYAKAAKAE--KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
AAY82573 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                       28-JUL-2000 (first entry)
                                                                                                                                                                                                           AAY82573;
                                                                                                                   RESULT 3
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         weight TV-marker polypeptides from the present invention. The present invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include archritic conditions, antibody-mediated diseases. Such diseases include archritic conditions, clempelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves include host-versus syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and cellayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physpetides which are analogous to allowed the contact of the contact of the molecules which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antianflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidametory condition; mementatic; antipsoriatic; dermatological; antianmatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                             AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                               Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.1%; Score 134.5; DB 21; Length 56; 68.4%; Pred. No. 6.2e-08; ive 0; Mismatches 5; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAEAKY - KAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82575 standard; peptide; 77 AA
                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 14; 72pp; English
                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
                                                                                                                  98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.1%;
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                             99WO-US22402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular weight markers
                                                                                                                                                                                                                                                          WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AA;
WO200018794-A1
                                                                                                                                                                                                                 3ad A, Lis D;
                                                                                                                  25-SEP-1998;
                                                                             24-SEP-1999;
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                                         06-APR-2000
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic unacemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chonic immune thyroiditis, autoimmune uveoretinitis, crohn's disease, chonic immune thyroiditis, autoimmune cuerated purpura, collitis, context sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, peoriasis, pemphigus vulgaris, or systemic line arthritis and endiated mediated medi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.
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Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
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Pred. No. 2e-07;
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                                                         pemphigus vulgaris; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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RESULT 6

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight. TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody-mediated diseases. Such diseases include architic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthitis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myaschenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                           glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyroimmetic; haemostatic; antipsoriatic; dermaclogical; antiannemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crowl disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; duillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                         Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuropro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                              Unidentified
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Gaps
                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                               41;
                             59.4%; Score 126.5; DB 21; Length 86; 45.3%; Pred. No. 7.1e-07; ive 0; Mismatches 6; Indels 41;
                                                                                                1 AKKYAKK----AKAEKA----KKAYKAAEAKKAAKYE--
                                                                                                                                                                30 -----KAAAEKAAAKEAAYEA 45
                                                                                                                                                                                    39; Conservative
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86 AA;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune cideases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, cantibody-mediated diseases. Such diseases include arthritic conditions, cantemia, autoimmune ophoritis, autoimmune haemolytic ansemia, autoimmune ophoritis, autoimmune thrombocytopaenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves CP disease, Guillain-Barre's syndrome, Hashimoto's disease, midiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated colinclude host-versus-graft disease, graft-versus-profiles of the invention have defined molecular weights and physical properties of the invention have colling makes them ideal for use as
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                                                                                                                                                                                                glatitamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antichyroid; antinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                           Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
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                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease;
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                   AAY82574 standard; peptide; 66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English.
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Best Local Similarity 71...
The 32; Conservative
                                                                                                (first entry)
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                                                                                                  28-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                         AAY82574;
AAY8257
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic manana, autoimmune ophoritis, autoimmune thrombocytopaenia uvecretinitis, crohn's disease, dishement in a diabetes mellitus, graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves upropura, colitis, contact sensitivity disease, diabetes mellitus, or systemic lupus erythematosus. Mediated-mediated diseases, which can be treated include host-versus-graft disease, graft-versus-host disease, and include host-versus-graft disease, graft-versus-host disease, and include host-versus-graft disease, polypeptides of the invention have defined molecular weights and physical properties which are analogous to appropriet and properties which mare analogous to a constant and properties which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                            Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                                          29 AKKYAKAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA
                                                                                                                                                              AAY82571 standard; peptide; 35 AA.
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                                                                                                                                                                                                                                                          28-JUL-2000
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1:19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US461009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. sequences, originating from the S' linker sequence, in order that the COP-1 polypeptide may be claaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAB, KAK, EKA, KKA, YEA, AKA KEA, and AAA. The N-terminal alamine residue is left behind following CNBr cleavage of the fusion protein.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control ademyelhating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                 10;
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                                                                                                                                                                                                                                                                                                        Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
   Length 35;
                                                                                                                                                                                                                                                                          Recombinant copolymer 1-19, myelin basic protein analogue.
                                 Indels
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                                                                                             1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
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Pred. No. 0.00076;
4; Mismatches 7;
Score 108; DB 21;
Pred. No. 2.9e-05;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 12; 25pp; English.
                                                                                                                                                                          AAR06446 standard; protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 46.7%;
1 Similarity 58.3%;
28; Conservative
 50.7%;
ilarity 64.4%;
Conservative
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89US-0312541.
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                                                                                                                                                                                                                                           (first entry)
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 Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                          multiple sclerosis;
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Matches 28; Conserv
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17-FEB-1989;
                                                                                                                                                                                                                                           03-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Claim 3; Page 21; 32pp; English.
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                                                                                                       92WO-US03609
                                                                                                                          91US-0694983.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Conservative
                                                                                                                                            (UNIW ) UNIV WASHINGTON
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                  46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 AA;
                 Modified-site
                                                                                                       01-MAY-1992;
                                                                                                                          03-MAY-1991;
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                                                                 WO9219248-A
                                                                                    12-NOV-1992
                                                                                                                                                               Stahl PD;
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Best Local
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                                                                                                                                                  glycopeptide, mannose, mannosylated, glycosylated, mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image, alter; macrophage processing of antigen, MRC restration; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; mononuclear pageoxytes; HIV; albS; lysosomal storage diseases; gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver; alveolar macrophages, prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucose
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                                                                                                                                  High affinity macrophage mannose receptor ligand compound #9.
                                                                                                                                                                                                                                                                                                    N-Ac-glucosamine. May also have non interfering substits."
         41
                   "opt may have mannose, fucose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "opt may have mannose, fucose,
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N-Ac-glucosamine."
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N-Ac-glucosamine."
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        KYAKKA-KAEKAKKAYKAAEAKKAAKYEKAAAEKAA-
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                                                                         AAR28871 standard; peptide; 46 AA.
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/note=
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/note=
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/note= |
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/note= '
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                                                                                                                23-MAR-1993
                                                                                                                                                                                                                                                    Synthetic.
                                                                                            AAR28871;
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This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on manocytes. Greeptors are uniquely found on macrophages and not on manocytes. Glycopeptides such as this provide a mechanism to target macrophages can display to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Orbhn's diseases infectious diseases in which macrophages harbour replicating infectious agents eg. Legionnaires disease; viral infections involving mononuclear phagocytes eg. HIV and lygosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease; asthma mediated by systemic macrophages; and in controlling metastasis, mediated by systemic macrophages to a marshal an immune response; also self peptides to marshal an immune response; also self peptides to marshal an immune response; also self peptides to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                or
/note= "opt may have mannose, fucose, glucose or
N-Ac-glucosamine."
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                                                                                                glucose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New high affinity mannose receptor ligand cpds. - for traiseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. HIV
                                                                                          /note= "opt may have mannose, fucose, g
N-Ac-glucosamine. May also have
interfering substits."
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63.4%; Pred. No. 0.00047;
iive 1; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA
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coding for rCOP-1-77 were subclosed from pREV 2.1 to pBG3-2deltaN (deposit: 20-NoV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode funion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. C. sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. C. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune complainmyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial ceffects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing genes encoding random polymers of aminoacid(s) - 1 producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.1%; Score 94; DB 11; Length 154; 60.5%; Pred. No. 0.0044; ive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 KKYKKKAKKAKKAKYKK--KAKEAEKA----KAAAEAEKAKEAEYK 141
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                                                                                                                                                90US-0473845.
89US-0312541.
                                                                                     90EP-0301700.
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les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological activity
                                                                                                                                                                                                                                     (REPL-) REPLIGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ05664
                                                                                     16-FEB-1990;
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17-FEB-1989;
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                              22-AUG-1990
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein canced by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and constitution the genome sequence and proteins encoded by the are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Monte. The general date of the treatment or prevention of infections by L. Monte. The desired date of the present of the present
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                                                                                                                                                                                                                                                                                                Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                 Dehoux P;
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                                                                                                                                                                                                                                                     Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entlan K, Hauf J; Posea M, Vorg L.
                                                                                                                                                                                                                                                                                                                                                                                  Durant L;
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Immunological activity; autoimmune encephalomyelitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID No 1828; 192pp; French.
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Daningle J., Goere.
Domingles-Bernal G, Garriuc
Chakraborty T, Domann E, Hr
Perez-Diaz J, Baquero F, G
Maduenio E, De Pablos B, I
                                                                                  11-APR-2001; 2001WO-FR01118.
                                                                                                                                             11-APR-2000; 2000FR-0004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W. vaccae proteins. The many vaccae proteins may be employed to activate or cells and natural killer cells, to stimulate the production of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant can function. The proteins can be expressed by standard recombinant can function. The proteins can be expressed by standard recombinant nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases immune disorders and cancer. In particular, the compounds and the methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as posiasis, atopic dermatitis, eczema, allergic contact dermatitis, alopecia areata, and skin cancers such as basal carcinoma, squamous cell carcinoma and melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides heat-killed Mycobacterium vaccae, or recombinant
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Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis;
perinuclear anti-neutrophil cytoplasmic antibody.
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42.7%; Score 91; DB 20; Length 223;
Best Local Similarity 59.6%; Pred. No. 0.014;
Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                    Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
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                                                                                                                                                                                                                                                                                                                                                                               Enhancing immune response to an antigen
                                                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 239; 243pp; English.
                                                              98US-0205426.
97US-0996624.
97US-0997080.
97US-0997362.
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98US-0156181.
                       98WO-NZ00189.
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                       23-DEC-1998;
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                                                                                                                                                                            17-SEP-1998;
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23-DEC-1997
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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a porini antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antigen, or the pANCA-reactive fragment, anti-neutrophil cytoplasmic antigen, or the pANCA-reactive fragment, complex of the histone H1-like antigen; and (3) detecting the and antibody to the histone H1-like antigen; and (3) detecting the antigen, because that the subject has UC. The pANCA-reactive histone H1-like antigen are useful in the antigen, porin antigen and Bacteroides antigen are useful in the diagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence
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pANCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein;
histone H1; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                               Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
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                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 11; 134pp; English
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97US-0837058.
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hes 25; Conservative
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                           WPI; 1999-551215/46.
                                                                       Cohavy 0;
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polypeptide (II) sequences. (II) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to rescree normal activity of (II) or to treat diseases states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                   designated 214.
                                  The invention provides a method for diagnosing ulcerative colitis in a
                                                    subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative collits. The method is used to diagnose ulcerative collits are method is used to diagnose represents a histone HI-like protein of M. tuberculosis, designated 21
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                         Score 89.5; DB 21; Length 214;
Pred. No. 0.019;
4; Mismatches 13; Indels 3
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                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 59052; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #28684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG28693 standard; Protein; 334 AA
Example 5; Fig 10; 49pp; English.
                                                                                                                                                                                                                                             42.0%;
55.6%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                              Local Similarity 55.6 tes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                          214 AA;
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                                                                                                                                                                                                          Sequence
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ABG28693
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                           Score 87; DB 22; Length 334;
Pred. No. 0.056;
6; Mismatches 12; Indels
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Best Local Similarity 57.4%;
Matches 27; Conservative
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Search completed: March 10, 2003, 12:21:28 Job time : 24.4494 secs

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/cgn2_6/ptodata/1/pubpaa/NCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/NCG_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                    188354 segs, 42170167 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Result No.	Score	Query	Query Match Length DB	DB	ID	Description	
	213	100.0	45	10	US-09-816-989A-2	Sequence 2, At	Appli
7	138	64.8	109	10	US-09-816-989A-7		App 1
m	134.5	63.1	56	10	US-09-816-989A-3	m	Appli
4	131	61.5	77	10	US-09-816-989A-5	'n	Appli
2	126.5	59.4	98	10	US-09-816-989A-6	9	Appli
9	120.5	56.6	99	10	US-09-816-989A-4	4	App1
7	108	50.7	35	10	US-09-816-989A-1	Ή,	Appl j
80	91	42.7	223	0	US-10-051-643-201	Sequence 201,	App
6	82	38.5	•	σ	US-09-738-626-5751	Sequence 5751, Ap	Ap
10	78	36.6	309	σ	US-09-820-843A-24	Sequence 24, A	Appl
11	75.5	35.4		10	US-09-923-304-2	Sequence 2, A	Appli
12	75.5	35.4	265	10	US-09-925-302-559	Sequence 559, Apr	Apr
13	74	34.7	352	σ	US-09-820-843A-23	Sequence 23, A	Appl
14	74	34.7		σ	US-09-820-843A-27		Appl
15	72.5	34.0		σ	US-09-820-843A-8		pji
16	70.5	33.1	619	σ	US-09-882-774-1		Ď11
17	70	32.9	641	10	US-09-765-272-160	Sequence 160, Apr	Apr
18	70	32.9	1156	10	US-09-815-242-13187	Sequence 13187,	7, 7
19	68	31.9	241	10	US-09-938-803-8	Sequence 8, Appli	ilaa

Sequence 7, Application US/09816989A, Patent No. US20020115103A1, GENERAL INFORMATION:
APPLICANT: Gad, Alexander APPLICANT: Lis, Doris

US-09-816-989A-7

	Sequence 4893, Ap Sequence 233, App Sequence 105, App Sequence 11554, A Sequence 11216, A Sequence 3188, Ap
	10 US-09-815-242-4893 10 US-09-764-846-233 12 US-10-007-693-105 10 US-09-815-242-11554 10 US-09-815-242-11216 10 US-09-815-242-11216 10 US-09-816-242-11316
2008 8454 8454 8454 8454 8454 8454 8454 8	782 379 656 829 850
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8 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 4 4 4 4 4 4 4 4 3 9 9 9 9 9 9 9 9 9 9 9

# ALIGNMENTS

Sequence 2, Application US/09816989A Patent No. US20020115103A1

JS-09-816-989A-2

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CURRENT APPLICATION NUMBER: US/09/816,989A
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Matches
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK FILLS OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-A-P-CT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR PAPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1999-09-24 SPRIOR FILING DATE: 1999-09-24 SEQ ID NOS: 7 SEQ ID NOT: 1098-09-24 SEQ ID 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORNATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION UNMERR: US/09/816, 989A
CURRENT FILLING DATE: 1090-03-25
PRIOR APPLICATION NUMBER: 60/101, 693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
COFTWARE: PARENTIN VERSION 3.1
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.8%; Score 138; DB 10;
Best Local Similarity 76.6%; Pred. No. 3.6e-08;
Matches 36; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09816989A
Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 68.4%;
Matches 39; Conservative
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ORGANISM: Artificial Sequence
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LENGTH: 56
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APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COFOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION TO BATE: 2001-03-23
PRIOR PELIOR DATE: 1999-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 АККУАККЕКАУАККАБКААККАБАКАУКАВЕАКККАКАВЕАККУАКААКАБККЕУАААБАК 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAEAKKKAKAEAKKYAKAAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.4%; Score 126.5; DB 10; Best Local Similarity 45.3%; Pred. No. 4.5e-07; Matches 39; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 61.5%; Score 131; DB 10; Local Similarity 50.6%; Pred. No. 1.4e-07; NB 39; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PELLING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ TO NO 5
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ҮКАЕААККАҮКАЕААКААКЕААУЕА 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09816989A
Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 -KAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YKABAAKAAKBAAYBA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-816-989A-4
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           of Immunologically-Mediated Diseases of the Respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 91; DB 9; Length 223
59.6%; Pred. No. 0.0059;
tive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKATAAKKATAATKA 183
TITLE OF INVENTION: of Immunologically-Mediated Diseases;
TITLE OF INVENTION: System using Mycobacterium Vaccae;
FILE REFERENCE: 11000 100802.
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
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Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EAITEKKKKAREDKEAKEAA--EKAAAEKAAAES 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 KAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/28098
PRIOR APPLICATION NUMBER: JP 00/28098
PRIOR APPLICATION NUMBER: JP 00/28098
SPIOR PILING DATE: 2000-08-03
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 5791
LENGTH: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OZAKI, AKIO
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5751, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09820843A; Publication No. US20030039963A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium vaccae US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 59.6'
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-820-843A-24
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                                 APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 00/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHILIN VERSION 3.1
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 00/101,693
PRIOR APPLICATION NUMBER: 00/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PATENTING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PATENTING DATE: 00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/101,00/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.6%; Score 120.5; DB 10; Length 66; ilarity 71.1%; Pred. No. 1.4e-06; Conservative 0; Mismatches 6; Indels 7
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Publication No. US20020197265A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
ITILE OF INVENTION: Methods and Compounds for the Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 32; Conserv
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US-10-051-643-201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 66
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Indels

Length 265;

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Wig-09-820-843A-23

Sequence 23, Application US/09820843A

Sequence 23, Application US/09820843A

Publication No. US2003003963A1

GENERAL INFORMATION:

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN

TITLE OF INVENTION: USEPUL AS ANTI-INFECTIVES

TITLE OF INVENTION: USEPUL AS ANTI-INFECTIVES

CURRENT APPLICATION NUMBER: US/09/820,843A

CURRENT PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.0

SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09820843A

Sequence 27, Application US_030039963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Council Of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Petentin version 3.0

SEQ ID NO 27
                                                                         FEATURE:

NAME/KEY: SITE

LOCATION: (4)

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-559
                                                                                                                                                                                                                                                                                                                                                    213 AKKITAASKKAPAQKVPAQKATGQKAAPAAQKGQKAPAQKADAPKAS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.7%; Score 74; DB 9; Length 352; 51.1%; Pred. No. 0.56; tive 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                             160 AKPAAKPAAKPAAKPAAKTAAAKPAAKPTAKPAAKPAAKTA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KRY: misc feature
NAME/KRY: misc feature
NAME/KRY: misc feature
NAME/KRY: misc feature
OTHER INFORMATION: gi|9951563
                                                                                                                                                                                                                          Query Match 35.4%; Score 75.5; DB 10; Best Local Similarity 51.0%; Pred. No. 0.29; Matches 25; Conservative 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: tolA protein
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9656364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 51.1
Matches 23; Conservative
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ORGANISM: Vibrio cholerae
                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-820-843A-27
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          LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 352
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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTMARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 309
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Patent No. US20020081612A1
GENERAL INFORMATION:
APPLICANT: KATZ.
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS;
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS;
TILE REPERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT PILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2.
LENGTH: 220
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                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
CTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF;
NAME/KEY: misc_feature
;
CTHER INFORMATION: gi|9951352
US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75.5; DB 10; Length 220;
Pred. No. 0.24;
7; Mismatches 10; Indels 7
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Fatent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78; DB 9; Length 309;
Pred. No. 0.19;
0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.8%;
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-2
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Best Local Similarity
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Gaps

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Sequence 8, Application US/09820843A
Sequence 8, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 372
TYPE: PRT
CORGANISM: H. influenzae
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                                            Query Match 34.7%; Score 74; DB 9; Length 356; Best Local Similarity 45.5%; Pred. No. 0.57; Matches 20; Conservative 4; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

CTHER INFORMATION: outer membrane integrity protein (tolA)

NAME/KEY: misc_feature

CTHER INFORMATION: gi|1573353

US-09-820-843A-8
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US-09-820-843A-27
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US-09-820-843A-8
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Search completed: March 10, 2003, 12:53:42 Job time : 13.5289 secs

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USA
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39, Appl
36, Appl
37, Appl
37, Appl
37, Appl
37, Appl
38, Appl
38, Appl
38, Appl
39, Appl
30, Appl
30, Appl
31, Appl
31,
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                                                                                                                                                                                      March 10, 2003, 12:15:04 ; Search time 7.97468 Seconds
    (without alignments)
166.029 Million cell updates/sec
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Sequence 1
Sequence 3
Sequence 3
Sequence 2
Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-205-426-201

US-09-041-889-39

US-09-041-889-38

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US-09-041-889-38

US-09-041-889-3

US-08-041-889-3

US-08-041-889-3

US-08-31-058-3

US-08-31-058-3

US-08-31-055-15

US-08-31-055-15

US-08-31-055-16

US-08-31-055-16

US-08-31-055-16

US-08-31-055-11

US-08-31-055-11

US-08-31-055-11

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US-08-31-055-11

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US-08-31-055-11
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US-08-839-624-26
US-09-150-812-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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213
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                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                              Run on:
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No.
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Appli
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Sequence 4,
Sequence 4,
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Sequence 2,
Sequence 3,
Sequence 3,
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Sequence 5,
Sequence 5,
Sequence 4,
Sequence 2,
Sequence 2,
               Sequence
                  US-08-837-058-4
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US-08-46-201-4
US-08-469-434-4
US-08-27-22-4
US-08-27-451A-5
US-08-28-346-8
US-08-28-346-8
US-08-293-284A-2
US-08-293-284A-2
US-08-21-164-2
US-08-21-164-2
US-08-21-164-2
US-08-21-164-2
US-08-21-164-2
                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS SOFTWARE: EASTER FASTER FOR THE ADPLICATION DATA: APPLICATION NUMBER: US/09/095,855
                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11000.1002c3
                                                                                                                                                                                                                                                                                                                                                            201:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Sequence 39, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.0%; Score 89.5; DB 3; Length 214; 55.6%; Pred. No. 0.0067; tive 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 41
CORRESPONDING ADDRESS:
CORRESPONDING ADDRESS:
CAMPAGESE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
TELEFAX: (419) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PILING DATE: 11-APR-1997
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 103 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: peptide
US-09-041-889-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.64
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTRY: USA
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      FILING DATE
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Fatent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                7
                                                                                                                                Gaps
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                                                                                                                                5,
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 201, Application US/09205426

Sequence 201, Application US/09205426

Sequence 201, Application US/09205426

GENERAL INFORMATION:

APPLICANT: Wateson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT APPLICATION NUMBER: 09/095,855

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER FILING DATE: 1997-06-12

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/705,347

EARLIER FILING DATE: 1997-06-12

EARLIER APPLICATION NUMBER: 08/705,347

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 223
                                                                  Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.7%; Score 91; DB 4; Length 223; Best Local Similarity 59.6%; Pred. No. 0.0048; Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                          12; Indels
                                                                                                                                                                                                                             137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAAPAKKAATKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                           Query Match
42.7%; Score 91; DB 4;
Best Local Similarity 59.6%; Pred. No. 0.0048;
Matches 28; Conservative 5; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-09-205-426-201
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STATE: California
COUNTRY: USA
ZIP: 92122
US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-205-426-201
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Gaps

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ZIP: 92122
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09041889
Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 158 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-041-889-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-041-889-3
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APPLICANT: Braun, Jonathan
APPLICANT: Braun, Jonathan
APPLICANT: Charay, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
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                                                Gaps
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36.2%; Score 77; DB 3; Length 103;
52.2%; Pred. No. 0.068;
iive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.2%; Score 77; DB 3; Length 116; Best Local Similarity 52.2%; Pred. No. 0.077; Matches 24; Conservative 1; Mismatches 13; Indels
                                                                                       51 AKPKAKKAGAAKAKKPAGATPKKAKKAAGAKKAVKKTPKKAKKPAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAKAEKA----KKAYKAAEAKKAAKYEKAABEKAAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-041-889-40
; Sequence 40, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Chavy, Offer
; TITLE OF INVENTION: Diagnosis, Prev
; TITLE OF INVENTION: Ulcerative Col:
                                                                                                                                                                                                                   US-09-041-889-38
; Sequence 38, Application US/09041889
; Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 amino acids
Query Match 36.2
Best Local Similarity 52.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-041-889-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE: 11-APR-1997
ATONEY/AGENT INPORMATION:
ATONEY/AGENT INPORMATION:
NAME: Campbell, Cathyn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-PM 3006
TELEPHONE: (619) 535-9001
TELEPRATION EN (619) 535-9001
TELEPRATION POR SEO ID NO: 40: SEQUENCE CHARACTERISTICS:
LENGTH: 158 anino acids
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APPLICANT: Braun, Jonathan
APPLICANT: Braun, Jonathan
APPLICANT: Chavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatn
TITLE OF INVENTION: Ulcerative Colitis, and Clinical
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
TITLE OF INVENTION: Microbial UC pANCA antigens NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
36.2%; Score 77; DB
Best Local Similarity 52.2%; Pred. No. 0.11
Matches 24; Conservative 1; Mismatches
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) OTHER INFORMATION: /note= "product = Human Histone ; OTHER INFORMATION: H1-S-3" US-08-837-058-3
                                                                                         Query Match 36.2
Best Local Similarity 52.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-09-041-889-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 24;
                                                                                                                                                                                                                                                                                             RESULT 9
US-09-041-889-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.2%; Score 77; DB 3; Length 222; Best Local Similarity 52.2%; Pred. No. 0.15; Matches 24; Conservative 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKAKAEKA-----KKAYKAAEAKKAAKYEKAAEKAAA 38
                                                                                                                                                                                                                                                                                                                                                                                  /note= "product = Human Histone
H1-S-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Catchyn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUTICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR EGN IN NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acide
TYPE: amino acide
TYPE: amino acide
                  FILING DATE: 11.APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER.STICS:
LENGTH: 222 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-00-837-058-3
; Sequence 3, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Targan, Stephan R.;
; TITLE OF INVENTION: Diagnosis, Pre;
; TITLE OF INVENTION: Uncerative Col, TITLE OF INVENTION: Uncerative Col, TITLE OF SEQUENCES. 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LIP
STREET: 4370 La Jolla Village Dr
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide
LOCATION: 1..222
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
LOCATION: 1..222
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Sequence 32, Application US/09041889
Fatent No. 6033864
GENERAL INFORMATION:
FALLCANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
FITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
FITLE OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: California
CONNTRY: USA
                                              <del>,</del>
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                                              Gaps
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36.2%; Score 77; DB 3; Length 222;
52.2%; Pred. No. 0.15;
ive 1; Mismatches 13; Indels
                                                                                                                             118 AKPKAKKAGAAKAKPAGATPKKAKKAAGAKKAVKKTPKKAKKPA 163
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                                                                                          ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ 1D NO: 32: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY, AGENT INFORMATION:
NAME: Campbell, Cathron A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-152-488-13
; Sequence 13, Application US/08152488
Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 226 amino acids
amino acid
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17.304-13

Sequence 17.304-14

Fatent No. 57371212

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN ANTICOACULAR WEIGHT STATE: New Jersey CONFORTS: States of America STATE: New Jersey CONFORTS: United States of America STATE: New Jersey CONFORTS: IDM PC COMPUTER FEADABLE FORM: MEDION GISK COMPUTER: IEBM PC COMPUTED: GONFORTS: NS-DOS; SOFTWARE: WORDPERFECT 6; ASCII (DOS) Text
CITY: Detroit

STATE: Michigan

CONTRY: United States of America

ZIP: 4826-4415

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS v. 6.22

SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,025

FILING DATE: 08-SEPT-1994

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US/08/303,025

FILING DATE: 14-A0G-1992

APPLICATION NUMBER: US 08/152,488

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROHM, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231

TELECOMMUNICATION INFORMATION:

MAME: ROHM, Benita J.

REFERENCE/DOCKET NUMBER: 7MH-060548-00231

TELECHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) DOCTOMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: pept:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-677-304-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-303-025-15
Sequence 15, Application US/08303025
Sequence 15, Application US/08303025
Patent No. 5614494
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
                                   James C.
NOVEL PEPTIDES FOR HEPARIN AND
LOW MOLECULAR WEIGHT HEPARIN
ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                              STATE: New Jersey
STATE: New Jersey
ZONUTRY: United States of America
ZIP: 07016-1818
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DGS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-NG-1993
ATTORNEY, AGENT INFORMATION:
NAME: ROHM, Benita J.
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 23,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                       TITLE OF INVENTION: NOVEL PEPTIDES
TITLE OF INVENTION: LOW MOLECULAR W
TITLE OF INVENTION: LOW MOLECULAR W
TITLE OF INVENTION: ANTICOAGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-13
           Philip C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE: N/A PUBLICATION:
           Andrews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserv
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Gaps
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Pred. No. 0.038;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER: Library diskette 3.5" 1.44Mb
COMPUTER: TBM PC Comparible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6:1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEBT-1994
                  APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROIM, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/POCKET NUMBER: 7WK-060548-00233
TELEPHONE: 313-965-1976
TELEPHONE: 313-965-1976
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTONEY/AGENT INFORMATION:
NAME: ROHM, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AKKA-AKKAKKA--AKKAKKAAKKAKKAKKA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAEKA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-303-025-16; Sequence 16, Application US/08303025; Sequence 16, Application US/08303025; Patent No. 5614494; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.0
Best Local Similarity 68.8
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
US-08-436-703B-2
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: N/A MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: Staniery, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Benita J', Rohm, Esq.
STREET: 6601 Woodward Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREEF: SULC.

CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MordPerfect 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
FILING DATE: 184
             APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIFICATION NUMBER: US/08/152,488
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAMME: ROAM: Benita J.
REGISTRATION NUMBER: 28,664
RECISTRATION NUMBER: 28,664
RECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-53344
INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH 32 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AKKA-AKKAKKA--AKKAKKAAKKAKKAKKA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acide
TYPE: amino acide
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORIGINAL SOURCE:
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE: N/A PUBLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-677-304-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-436-703B-2
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SEQUENCE THANKTHESTICS:

LEWOTH: 31 anno acide
TTRE: MAN anno acide
TTREE TREET: MAN anno
TTREET: MAN ANNO
TTREET
TTREET: MAN ANNO
TTREET
TTREET: MAN ANNO
TTREET:
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; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
US-08-436-703B-4

Query Match
Best Local Similarity 68.8%; Pred. No. 0.039;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAKAEKAKKAAKKAAKKAAKKAAKKA 36

Qy 5 AKKAKAKA-AKKAKKAAKKAAKKA 31

Db 3 AKKA-AKKAKKA-AKKAKKAAKKAAKKA 31

Search completed: March 10, 2003, 12:30:02
Job time: 8.97468 secs
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein March 10, 2003, 12:15:04; Search time 16.4219 Seconds (without alignments) 327.825 Million cell updates/sec Run on:

US-09-816-989A-3 266 Perfect score:

1 AKKYAKKEKAYAKKAEKAAK.........BAKYKAEAAKAAAKEAAYEA 56 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Bummaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tolA protein - Esc	hypothetical prote	ㅁ	membrane spanning	tolA protein [impo		outer membrane int	histone H1 - sea u	TolA protein PA097	histone H1-beta, e	sperm tail-specifi	histone H1 - rainb	hypothetical prote			repetitive protein	outer membrane pro	histone H1-gamma,	histone H1, gonada	probable translati	Tola colicin impor	probable hupB - My	e t	zuotin - yeast (Sa	kinase-like protei	histone H1 homolog	R27-2 protein - Tr	histone H1.10 - ch	histone H1 - wheat
SUMMARIES	ΩI	JV0057 .	AE1317	F90725	G85576	AG0592	T09127	G64064	A25550	E83525	A28100	851364	HSTRIR	AE1689	T17698	809388	E60110	B43592	A26721	HSUR1P	T11583	AC0138	G70673	A44993	\$25194	T48600	S61926	T30296	$^{\circ}$	S22322
	DB	7	7	~	~	~	~	N	N	N	~	~	ч	~	N	N	7	~	~	н	~	~	~	7	~	N	~	~	N	7
de	Length	421	239	394	394	376	1701	372	210	347	211	1390	206	243	311	206	219	384	217	248	1403	388	214	328	433	703	182	1128	220	236
	Query Match	44.0	43.8	42.5	42.5	41.5	41.4	39.7	38.5	38.5	38.3	37.8	37.4	37.0	37.0	36.7	36.5	36.1	•	35.9	35.9	35.7	35.5	35.5	35.3	35.3	34.8		34.6	34.6
	Score	117	116.5	113	113	110.5	110	105.5	102.5	102.5		100.5	99.5	98.5	œ	97.5	97	96	95.5	95.5	95.5	95	4	94.5	94		ď.	92.5	92	92
	Result No.	п	7	m	4	ß	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 AE1317

histone H1-delta -	histone H1-II - Vo	conserved hypothet	IgA-specific metal	histone H1 - Chlam	immediate-early pr	translation initia	probable late embr	histone H1 - trout	tolA protein VC183	arylesterase-relat	hypothetical prote	hypothetical prote	histone H1 (clone	hypothetical prote
A32137	JN0748	E75383	A26039	859589	EDBEQ3	AI0424	T14305	HSTR1	A82152	G87675	T32633	T34010	T06257	T03561
20	4 (4	N	~	N	н	~	7	Н	N	N	0	N	~	N
185	241	581	1532	231	407	884	136	194	356	438	1655	1482	288	461
34.4	34.2	34.0	34.0	33.8	33.8	33.8	33.6	33.6	33.6	33.6	33.5	33.3	33.1	33.1
91.5	91	90.5	90.5	90	90	90	89.5	89.5	89.5	89.5	89	88.5	88	88
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C.Accession: 070057; B64810
B.Levengood, S.K.; Webster, R.B.
J. Bacteriol. 171, 6600-6609, 1989
A.Fitle: Nucleotide sequences of the tola and tola genes and localization of their produc
A.Reference number: 070057; MUID:90078104; PMID:2687247
                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-421 cLEV.

A; Residues: 1-421 cLEV.

A; Cross-references: GB:M38232; NID:g148018; PIDN:AAA24683.1; PID:g148019

A; Cross-references: GB:M38232; NID:g148018; PIDN:AAA24683.1; PID:g148019

A; Experimental source: strain JM105

A; Note: the authors translated the initiation codon GTG for residue 1 as Val

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Richer Complete genome sequence of Escherichia coli K-12.

A; Attle: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Status; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11arity 54.7%; Pred. No. 0.0043;
Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CiReywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS> F;76-301/Domain: helical #status predicted <HSR> F;35-362/Region: nucleotide-binding motif A (P-loop)
tolA protein - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 17 min
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:209 A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics: A;Gene: tolA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cold protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18 C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AG0592 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Churcher, R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Churcher, S.; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference of a multiple drug resistant Salmonella enterica serove.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1225, 1998
A;Titles A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: 216577; MUID:98115903; PMID:9448314
A;Accession: T09127
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 376;
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                                                                                                                                                                                                                                                                                                               Length 394;
                                                                                                                                                                                                                                                                                                     Score 113; DB 2; Length 35
Pred. No. 0.0088;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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A;Residues: 1-1701 <KAP>
A;Cross -references: EMBL.AF031886; NID:92947227; PID:92947228
A;Experimental source: subspecies yoelii; strain YM
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llarity 53.5%; Pred. No. 0.014;
Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110; DB 2;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%;
Matches 33; Conservative
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54.2%;
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nes 38; Conserva
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-376 < PAR>
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Best Local Similarity
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Matches
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: P90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Vasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gA;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-239 <GLA>
A,Cross-references: GB:NC 003210; PIDN:CAD00019.1; PID:g16411394; GSPDB:GN00177
A,Experimental source: strain EGD-e
C,Genetics:
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A; CHAY>
A; CHAY>
A; CHAY>
A; CHAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55
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60.0%; Pred. No. 0.0088;
iive 5; Mismatches 11; Indels
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9; Mismatches 15; Indels
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108 33; Conservative
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83552
R;Stower, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olaon, M.Y.
J. Lory, S.; Olaon, M.V.
J. Lory, M. J. Lory, M.J. J. Lory, M.J. Lim, J. Lim, J. J. Lory, M.J. J. J. Lory, M.J. Lory, M.J. J. Lory, M.J. J. Lory, M.J. J. Lory, M.J. J. Lory, 
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C;Jate: 28-Aug-1999 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
R;Lai, E.C.; Childs, G.
A;Title: Characterization of the structure and transcriptional patterns of the gene encor A;Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 102; DB 2; Length 211; 44.8%; Pred. No. 0.046; ive 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102.5; DB 2;
Pred. No. 0.061;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KKKAAEEAKKKA-AAEAAKKKAAVEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 KKKA--EAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AE004530; GB
A,Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.5%;
Best Local Similarity 43.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 44.8%;
Conservative
                                                                                                                                                                                                                                                                                                            Tola protein PA0971 [imported]
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A,Residues: 1-211 <LAI>
A,Cross-references: GB:M20314
                                                                                                                  156 PAKKAAKKPAAKKA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: histone H1
                                           43 EAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 KPAAKKA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: tolA; PA0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A28100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
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Matches
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S51364
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histone H1 - sea urchin (Lytechinus pictus)

C;Species: Lytechinus pictus (painted urchin)

C;Decies: Jo-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999

C;Accession: A25550

R;Knowles, J.A.; Childs, G.J.

Rythowles, J.A.; Childs, G.J.

A;Knowles, Acids Res. 14, 8121-8133, 1986

A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an A;Reference number: A25550; MUID:87040778; PMID:3022245
                                                                                                                                                                                                                                                     RESULT 7
GG64064

GG64064

Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64064; UC5222
C;Accession: G64064; UC5222
R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.P.; Kerlavage, R;Pleischmann, R.D.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Ruhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Aritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; WUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; R;Sen, K.; Sikkema, D.J.; Murphy, T.F. Gene 178, 75-81, 1996
A,Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA A,Reference number: JC5212; MUID:97080550; PMID:8921895
A;Accession: JC5212
A;Accession: JC5212
A;Molecule type: DNA
       5
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                                                                                                                      96 KTEAQKARAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK 155
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                           5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA-----KYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
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A;Experimental source: strain 1479
A;Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-372 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.7%; Score 105.5; DB 2; Length 3 Best Local Similarity 48.2%; Pred. No. 0.036; Matches 27; Conservative 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Indels
   14; Indels
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Pred. No. 0.042;
5; Mismatches 1
5; Mismatches
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41.9%;
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Best Local Similarity 41.9
Matches 31; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-210 <KNO>
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A;Start codon: GTG
32;
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Matches
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4

31; Gaps

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C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S09388
R;Hill, C.S., Martin, S.R.; Thomas, J.O.
B;Hill, C.S., Martin, S.R.; Thomas, J.O.
B;Hill: A $251-2599, 1989
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chromany. Reference number: S09388; MUID:90060019; PMID:2583125
                ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                                        A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AE1689
A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-243 <GLA>
A;Residus: 1-243 <GLA>
A;Residus: Comparative control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein A208R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Accession: T17698
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17698
A;Accession: T17698
A;Accession: T17698
A;Accession: Library, translated from GB/EMBL/DDBJ
A;Accession: Library, translated from CB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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43.9%; Pred. No. 0.12;
ive 8; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96576.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 36.7%; Score 97.5; DB 2; Length 2 1. Similarity 52.6%; Pred. No. 0.11; 30; Conservative 3; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98.5; DB 2;
Pred. No. 0.1;
9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histone H1 - sea urchin (Parechinus angulosus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.0%;
50.0%;
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-206 <HIL>
C,Superfamily: histone H1
C,Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.03
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: 1in2055
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S09388
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C;Species: Drosophila hyde:
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
R;Neseen, J: Padmanabhan, S:; Buenemann, H.
Bur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A;Reference number: S51364; MUID:95045539; PMID:7957199
A;Accession: S51364
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
Hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001
C;Accession: AE1689
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karet, U.
Science 294; 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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histone H1 - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Spacies: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jun-2000
C;Accession: A02584 #sequence_revision N.J.; Dixon, G.H.
R;Mezquita, J.; Connor, W.; Winkfein, R.J.; Dixon, G.H.
A;Mol. Evol. 21, 209-219, 1985
A;Title: An H1 histone gene from rainbow trout (Salmo gairdnerii).
A;Reference number: A02584; MUID:85264847; PMID:6443128
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A, Reddues: 1-206 cMEZ.
A, Reddues: 1-206 cMEZ.
A, CCOSH CAB37646.1; PID: 94468016
C, Superfamily: histone H1
C, Superfamily: histone H2
C, Keywords: chromosomal protein; DNA binding; nucleosome
F;1-44/Region: flexible nose
F;45-117/Region: globular head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAKKEK--AYAKKAEKAAKKAEAKAYK----AAEAKKKAEAKYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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46.7%; Pred. No. 0.074;
tive 7; Mismatches 18; Indels
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Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-1390 «NEE>
A,Cross-references: EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
Swahitted to the EMBL Data Library, June 1993
A,Reference number: S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: FlyBase: FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.8%;
50.8%;
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A,Gene: mst101(2)
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Search completed: March 10, 2003, 12:28:27 Job time : 17.4219 secs

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# GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 12.7595 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

US-09-816-989A-3 266 1 AKKYAKKEKAYAKKAEKAAK......BAKYKABAAKAAAKEAAYEA 56 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ichia	hilus	albop	aegyp	inus	monas	hila	ynchu	Sumo	yloce	cteri	ema p	yloce	inus	sacch	s vul	cteri	romyc	cteri	gall	yloce	um ae	ella	omus	cart	omus	ria g	virus	ia pe	trutt	tendi	gall	tendi
	ption	escherichia	haemophilus	aedes albop	aedes aegyp	lytechinus	pseudomonas	drosophila	oncorhynchu	chironomus	strongyloce	mycobacteri	treponema	strongyloce	parechinus	schizosacch	proteus vu	mycobacteri	saccharomy	mycobacteri	gallus gall	strongyloce	-	_	_		chironomus	neisseria	herpesvirus	yersinia pe	salmo trutt	glyptotendi	gallus	glyptotendi
	Description		P44678	Q9u762	Q9u761	P06144	P50600	008696	P06350	P40278	P15869	99xb18	P29720	P07796	P02256	Q10475	09z£22	P95109	P32527	Q9zhc5	P08286	P15870	P27806	Q93mh5	P40277	208865	P40262	P09790	001042	Q8zbc2	P02254	P40266	P12957	P40263
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SUMMARIES		A ECOLI	A HAEIN	RS6 AEDAL	RS6 AEDAE	H1 LYTPI	A PSEAE	MST2_DROHY	H1_ONCMY	CHITE	STRPU	DBH_MYCBO	3 TREPH	STRPU	PARAN	YDF3_SCHPO	IF2 PROVU	MYCTU	I YEAST	MYCSM	H110 CHICK	STRPU	HEAT	KLEPN	CHITE	VOLCA	CHIPA	NEIGO	HSVSA	IF2_YERPE	SALTR		CHICK	GLYBA
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de	Query Match	44	39.7	39.5	39.3	38.5	38.5	37.8	37.4	37.4	37.2	36.7	36.1	35.9	35.9	35.9	35.7	35.5	35.3	35.2	34.6	34.4	34.4	34.2	34.2	34.2	34.0	34.0	33.8	33.8	33.6	33.3	33.1	32.9
•	Score		105.5	.105	104.5	102.5	102.5	100.5	99.5	99.5	σ	97.5	96	95.5	95.5	95.5	95	94.5	94	93.5	92	91.5	91.5	91	91	91	90.5	90.5	90		ď.	88.5	88	87.5
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MST1_DROHY H101_CHICK BDH2_STRCO H1B_GHITE TWPB_TREPA HCT1_CHLTR H1_ECHCR H1_CHICK H1O_CHICK TOPI_STRCO RSIG_BACTN H11_CABEL	
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# ALIGNMENTS

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MEDLINE=95350630; PubMed=7542800;
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RS6 AEDAL
ID RS6 AI
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                      SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                               SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                    Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                         X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.

MEDLINE=99312679; PubMed=10404600;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Filamentous phage infection: crystal structure of gjp in complex with its coreceptor, the C-terminal domain of TolA.";
Structure 7:711-72(1999).
-i- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 X TANDEM REPEATS OF [ED]-K(1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
         "Tola central domain interacts with Escherichia coli porins";
EMBO J. 15:6408-6415(1996).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.0%; Score 117; DB 1; Length 421; larity 54.7%; Pred. No. 0.0024; Conservative 5; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Inner membrane; 3D-structure; Complete proteome.
DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
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8B2F52B4B97C655E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AA; 43156 MW;
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EMBL; AEG00177; AAC73833.1; -.
EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
PDB; 1TOL; 20-MAX-99.
                                                                                                                                                                                                                                                                                                                                                             PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
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421
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278
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Tola OR HI0383.
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Lloubes R.;
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                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Lui L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hamma M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Protein transport; Transmembrane; Repeat; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V -> A (IN STRAIN 1479).
K -> R (IN STRAIN 1479).
A -> P (IN STRAIN 1479).
A -> R (IN STRAIN 1479).
V -> A (IN STRAIN 1479).
D -> A (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
L -> F (IN STRAIN 1479).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%; Score 105.5; DB 1; Length 48.2%; Pred. No. 0.019; tive 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I -> V (IN STRAIN 1479).
N -> S (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
S -> P (IN STRAIN 1479).
Z66ECFOSCGC95544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS6_AEDAL STANDARD; PRT; 349 AA Q9U762; 15-7UN-2002 (Rel. 41, Created) 15-7UN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
PERIPLASMIC
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                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19934; 1TOL.
TIGR; HI0383; -.
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27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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us-09-816-989a-3.open.rsp

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                                                                                                                                                                                                     SEQUENCE FROM N.A.
Gavino V.H., Fallon A.M.;
Gavino V.H., Fallon A.M.;
Gavino V.H., Fallon A.M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR CLASSES OF MRNA [By similarity].
-!- FTW: Ribosomal protein S6 is the major substrate of protein
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Gavino V.H., Fallon A.M.;

Gavino V.H., Fallon A.M.;

Gavino V.H., Fallon A.M.;

Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
CLASSES OF MRNA (By similarity).

-1- PTM: Ribosomal protein 86 is the major substrate of protein

kinases in eukaryote ribosomes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pteryguta; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
NCBI_TaxID=7159;
                                                                   Aedes albopictus (Forest day mosquito).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 kinases in eukaryote ribosomes (By similarity).
SIMILARITY: BELONGS TO THE SGE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein; Phosphorylation.
SEQUENCE 349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.5%; Score 105; DB 1;
46.5%; Pred. No. 0.02;
iive 7; Mismatches 13;
15-JUN-2002 (Rel. 41, Last annotation update) 40S ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S_ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD003460; Ribosomal S6E; 1. PROSITE; PS00578; RIBOSOMAL S6E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR001377; Ribosomal S6E.
Pfam; PF01092; Ribosomal S6e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF154066; AAF04789.1; -.
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315 KAAPAAKKEA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 EAAKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                               NCBI_TaxID=7160;
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AC AEDAE
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AC AEDAE
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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Knowles J.A., Childs G.J.;
Nucleic Acids Res. 14:8121-8133(1986).
-: FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-: SUBCELLULAR LOCATION: Nuclear.
-: SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
-1- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%; Score 104.5; DB 1; Length 346; 45.6%; Pred. No. 0.022; Live 5; Mismatches 17; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom, PD003460; Ribosomal_S6E; 1.
PROSITE, PS00578; RIBOSOWAL_S6E; 1.
Ribosomal protein; Phospbox_Istion.
SEQUENCE 346 AA; 39365 MW; 599CFF7B22BDBDFC CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         EMBL, AF154067; AAF04790.1; -. InterPro; IPR001377; Ribosomal S6E. Pfam; PF01092; Ribosomal S6e; 1.
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InterPro; IRR001386; Histone H1/H5.
InterPro; IRR001316; Linkerhist N.
Pfam, PR00539; Linker histone; I.
ProDom; P0000373; Linkerhist N; I.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
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Matches 31, Conservative
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PERIPLASMIC (POTENTIAL)

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                                                                                                                                            2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-------KKAEAKYKA 42
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
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                                                                                                     19; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                             Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                             DB 1;
                                                           Score 102.5; DB Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          347 AA.
                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U39558; AAC44660.2; -.
                                                             38.5%;
41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
                                                                                                   31; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                       156 PAKKAAKKPAAKKA 169
                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                              43 EAAKAAAKEAAYEA
                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                        TOLA PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                           Query Match
                                                                                                     Matches
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DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q.
                                                                                                                                                                                                                                                                                      31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                   ---YKAAE-A 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meesen J., Padmanabhan S., Buenemann H.; Meesen J., Padmanabhan S., Buenemann H.; Mandemly arranged repeats of a novel highly charged 16-amino-acid motifir representing the major component of the sperim-tail-specific aroneme-associated protein family Dhmstl01 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Figure 1 Specific Control of Specific Control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                         Length 347;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                       37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                    38.5%; Score 102.5; DB 1;
43.0%; Pred. No. 0.032;
tive 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Axoneme_associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%; Score 100.5; DE 50.8%; Pred. No. 0.15; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S34154; S34154.
FlyBase; FBgn0020733; Dhyd\mst101(2)
                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 KKKAAEEAKKKA-AAEAAKKKAAVEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 KKKA--EAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MST101(2).
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X73481; CAA51876.1; -.
                                                                                                                                                                                                                                                                                      37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
38 3
209 2
347 AA;
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila hydei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Local Si.
30;
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                                                                                            SEQUENCE
                                                                                                                                                                                              Query Match
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chironomus tentans (Midge).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEK-----AAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA 53
                                                                                                               Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach U.;
                                                                                                                                                                                                  MEDLINE=85564847; PubMed=6443128; MEZQLINE=85564847; PubMed=6443128; MeZquita J., Connor W., Winkfein R.J., Dixon G.H.; MeZquita J., Connor W., Winkfein R.J., Dixon G.H.; J. MoZ. D. 11.209-219 (1985).
-!- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEGOOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99.5; DB 1; Length 206;
Pred. No. 0.038;
7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION (BY SIMILARITY). GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72C440798066716C CRC64;
                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Histone Hib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 AA.
                                              206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P08287; IGHC.
InterPro; IPR001386; Histone H1/H5.
Pfam; PF00538; linker histone; 1.
ProDom; PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20672 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X02624; CAB37646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dest Local Similario,
Watches 28; Conservative
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 1
206 AA;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetylation.
INIT MET
MOD RES
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                                             H1 ONCMY
P06350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
HIE CHITTE
HIE CHITTE
DT 01-FE
DT 01-FE
DT 15-JU
DE Histo
OC Eukar
OC Eukar
OC Chirco
OC Chirco
OX NCBI
RN [1]
RP SEQUE
RA SCHUIL
                                  ONCMY
                      RESULT
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01-APR-1990 (Rel. 14, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
Histone H1-berta, late embryonic.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 AKKATKAAKPAAKKVAAKPAAKKAAAPKPKAAAKPKKEVKPKKEAKPKKAAAKPAKKPA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88246461; PubMed=2837660;
Lai Z.-C., Childs G.;
"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urchin Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLESCENDE CHARINS INTO HIGHER ORDER STRUCTURES.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR0013186; Histone H1/H5.
InterPro; IPR001316; Linkerhist N.
Promo; Pr00538; Linkerhist N.
Probom; PD000373; Linkerhist N; I.
SWART; SW00526; H15; I.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 237 AA; 24689 WW; D429364FFBCB1F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAA----EAKKKAEAKYKAEAAKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                  CONDENSATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases
                              -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE COND NUCLESCOME CHAINS INTO HIGHER ORDER STRUCTURES.
-1- SUBGELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L29105; AAB53945.1; -. HSSP; P08287; 1GHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.43
Matches 33; Conservative
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NCBI_TaxID=7668;
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                                                                                                                                                                                     from Mycobacterium.",
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- PUCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                               Gaps
                                                                                                                                                                         KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK------KKAEAKYKAEAAKAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prabhakar S., Tyagi J.S., Prasad H.K.;
"HLDMt-A target for differentiation of M.tuberculosis and M.bovis.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
           InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pram; PR00538; linker histone; 1.
ProDom; PD000373; LinKerhist N; 1.
SWART; SMOS26; H15; 1.
Chromosomal profein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 211 AA; 22169 WW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T., "Identification of a novel protein generating bacterial slow growth
                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                  DBH_MYCBO STANDARD; PRT; 205 AA.
995B18; 995B18; 995B18; 16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
10-0cT-2001 (Rel. 40, Last annotation update)
                                                                                                                   37.2%; Score 99; DB 1; Length 211; 44.8%; Pred. No. 0.042; tive 4; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO00113; Bac DNAbind.
InterPro; IPR001186; H18Tone_H1/H5.
Pfam; PF00216; Bac DNA binding; 1.
ProPom; PR00624; HISTONEH5.
ProPom; PD000045; Bac DNAbind; 1.
SWART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y18421; CAB46493.1; -.
EMBL; AB013441; BAA78330.1; -.
HSSP; P02346; 1HUU.
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BCG / Tokyo;
                                                                                                                   Query Match
Best Local Similarity
Matches 30; Conserv
 HSSP, P02259; 1HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     156 KPAAKKA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1765;
                                                                                                                                                                                                                            KEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=AN5;
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1-11.
1-13.
1-14.
1-15.
1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TupA and TupB proceins."; Infect. Immun. 59:3685-3693(1991).

-!- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR LARGE MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
[ED].
                                                                                                                Gaps
                                                                                                            3;
                                                                           Score 97.5; DB 1; Length 205; Pred. No. 0.055; Mismatches 15; Indels
                                                                                                                                                            2
 BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKE
                DEGENERATE REPEATS REGION.
A -> T (IN REF. 2).
19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB)
                                                                                                                                                                                                                                                                                                                                                             Treponema phagedenis.
Treponema pagedenis.
Bacteria, Spirochaetales, Spirochaetaceae, Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
                                                                     36.7%; Score . 0.055; 56.9%; Pred. No. 0.055; 4; Mismatches
                                                                                                                                                                                                                                                        384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; Outer membrane; Repeat; Signal.
                                                                                                                                                                                                                                                        PRT;
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MEDLINE-91372983; PubMed-1894368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-2.
11-3.
11-5.
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90 BA
205 DE
199 A
21262 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M58563; AAA27480.1; -. PIR; B43592; B43592.
                                                                                             l Similarity 56.9
29; Conservative
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
101
199
1205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=162;
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151
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                DOMAIN
CONFLICT
SEQUENCE
                                                                                Query Match
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135 AKKAAKKATKKTKKVKKPAAKKAKRPAAKKPAAKKPAAKKAFKKPAKKVAKPAKKAAAKPA 194
                                                                                                                                                                                                                                                                                                                   cyanogen bromide peptides.";
Bur. J. Biochem. 104:559-566(1980).
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                           195 KKAAKPAKKAA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AA;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 80-248.
                       42 AEAAKAAAKEA
                                                                                                                                                                                                                NCBI_TaxID=7658;
                                                                                                                                                                                                                                       SEOUENCE OF 1-84
                                                                                                                                                                                                       Parechinus.
                                                                                        H1_PARAN
ID_ H1_PARAN
AC P02256;
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7
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87172742; PubMed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; "Isolation, characterization, and expression of the gene encoding the late histone subtype HI-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                          Gaps
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                                                                                                                                             1 AKKYAKKEKAYAKKA--EKAAKK--AEAKAYKAAEAKKKA----EAKYKAEAAKAAAKEA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein, Nuclear protein, DNA-binding, Multigene family. SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 35.9%; Score 95.5; DB 1; Length 217; 1 Similarity 43.7%; Pred. No. 0.084; 31; Conservative 5; Mismatches 16; Indels 19;
                                                                                                 DB 1; Length 384;
                                                                                                                        17; Indels
                                                                             6E94CBC74294DE8C CRC64;
                                                                                                 Query Match 36.1%; Score 96; DB 1;
Best Local Similarity 51.6%; Pred. No. 0.12;
Matches 33; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                        217 AA
                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPRO01386; Histone H1/H5.
InterPro; IPRO03216; Linkerhist N.
Pfam; PPO0538; linker_histone; I.
 A-A-E
            ProDom; PD000373; Linkerhist N; 1.
                                                                             42677 MW;
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                                                                                                                                                                                                                                                                      STANDARD;
           243
252
261
270
279
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                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus.
NCBI_TaxID=7668;
                                                                           384 AA;
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          236
245
254
254
263
272
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238 ARKA 241
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Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
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                                                                                                                                                                                         Histone H1, gonadal. (Angulate sea urchin). Barechinua angulosus (Angulate sea urchin). Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 K -> R.
26387 MW; 1B25B3F136541947 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1002 (Rel. 41, Last annotation update)
Probable eukaryotic initiation factor Cl7C9.03.
                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
248 AA.
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01-OCT-1996 (
15-JUN-2002 (
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YDF3 SCHPO
TD YDF3 SCHPO
AC Q10475;
DT 01-OCT-1996
DT 15-UNZ-2002
DE Probable euks
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us-09-816-989a-3.open.rsp

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RA Wood V. Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
R. Brooks M., Brown D., Brown S., Chillingworth T., Churcher C.M.,
R. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
R. Collins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,
A. Holroyd S., Honsby T., Howarth S., McDonald S., McLean J.,
A. James K., Jones L., Jones M., Laather S., McDonald S., McLean J.,
A. Junes K., Jones M., Leather S., McDonald S., McLean J.,
A. Joher K., Jones M., Squares R., Squares S., Stevens K.,
A. Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A. Taylor K., Taylor K., Taylor K., Whithehead S.,
A. Taylor K., Taylor R., Taylor K., Muller B., Whithehead S.,
A. Moodward J., Volckaert G., Aerr R., Robben J., Grymonpraz B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
B. Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A. Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
B. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
A. Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
A. Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
A. Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
A. Shakory G.Y., Sanchez M., Sallardin J., Potashkin J.,
A. Shakovski G.V., Besty D., Barrell B.G., Nurse P.;
A. Shakovski G.V., Barsell B.G., Nurse P.;
A. Ann P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.9%; Score 95.5; DB 1; Length 1403; 44.3%; Pred. No. 0.38; 1.1ve 12; Mismatches 17; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1403 AA; 154034 MW; 0317EE65BE2A1E63 CRC64;
                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                               STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
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InterPro; IPR003890; IF eIF4G.
Pfam; PF02854; MIF4G; 1.
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Best Local Similarity 44.3*
                                                                                       Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                            SEQUENCE FROM N.A.
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Search completed: March 10, 2003, 12:17:09 Job time : 13.7595 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:01; Search time 29.654 Seconds (without alignments) 389.109 Million cell updates/sec

US-09-816-989A-3

Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL Database

sp\_archea:\* sp\_bacteria:\*

sp\_fungi:\*
sp\_human:\*
sp\_human:\*
sp\_nuvertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_plant:\*
sp\_plant:\*
sp\_vorganelle:\*
sp\_archeap:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q9cm70 pasteurella Q9y5w4 listeria mo Q937k4 erwinia chr Q8zqt6 salmonella Q8x965 escherichia Q93946 candida alb Q928c1 salmonella O6164 plasmodium Q8t5c8 plasmodium Q8xvn7 ralstonia s Q92a67 listeria in Q84528 paramecium Q9ndi9 plasmodium Q9uv33 ascobolus i Q9kj98 escherichia Q9wwx1 pseudomonas Description Q9WWX1 Q9CM70 Q957X4 Q937X4 Q8XQT6 Q8X20F6 Q8X365 Q8X861 Q8X787 Q8TSC8 Q8XW7 Q9XW7 Q9AD19 Q9WD19 Q9WD19 Length DB 394 212 376 1701 1866 200 243 311 969 629 Query Match 1 42.5 41.7 41.5 36.8 36.1 35.9 Score 1116.5 1113.5 1113.5 1110.1 110.1 110.5 100.5 98.5 98.5 96.5 Result Š.

Q9xh19 triticum ae Q8zgz2 yersinia pe Q9ylpg plasmodium Q46141 mytilus edu Q46142 mytilus edu Q46142 mytilus edu Q46142 mytilus edu Q46143 mytilus edu Q91ya2 arabidopsis Q98yg7 rhizobium 1 Q93ys6 arabidopsis Q45370 bordetella Q26947 trypanosoma Q8t5c9 plasmodium Q18319 chironomus Q91566 streptococc Q91az2 streptococc Q91az2 streptococc Q91az2 streptococc Q8t5c7 plasmodium	Ogswul triticum ae Qgswul triticum ae Q65794 triticum ae O46140 mytilus edu Q9ru45 deinococcus Q9fp71 oryza sativ Q9bmy8 leishmania Q8y1f6 ralstonia 8 Q39681 daucus caro Q9kr10 vibrio chol
10 Q9XHL9 16 Q8ZGZ2 20Y1P8 5 O46141 5 O46142 5 O46142 6 O46142 5 O46142 6 O46142 6 O46142 6 O46143 7 O46143 6 O46143 6 O46143 7 O46143 6 O46143 7 O46143 6 O11395 7 O4615 6 O11319 7 O4615 6 O1156 7 O4615 7 O4615 8	10 Q9SWU3 10 Q9SWU2 10 Q6SWU2 5 Q46140 16 Q9RU45 10 Q9FP71 5 Q9RNY8 16 Q8Y1F6 10 Q39681 16 Q9KR10
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## ALIGNMENTS

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MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
J. Bacteriol. 178:1699-1706 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96422022; PubMed=8824639;
doditjuez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                  Last sequence update)
                                                                          372 AA.
                                                                                                                                                             Created)
                                                                              PRT;
                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                     rolA protein.
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RESULT 1
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01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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Matches 32; Conservative
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Q937K4;
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Matches
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Q937K4
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Q8ZQT6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Chaquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Chatubit A., Chetouani F., Couve B., de Daruvar A., Deboux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautler L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006136; AAK03052.1;
HSSP; P19934; 1TOL.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 389;
                                                                                                       Score 117; DB 2; Length 372;
Pred. No. 0.0035;
2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.0%; Score 117; DB 16; Length 3 Best Local Similarity 55.9%; Pred. No. 0.0037; Matches 33; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                     113 RÉAAEAKKAEDAAKAAEAA--KAAEAKKAAEAKKADEAKKAAEKOOA 157
                                                                                                                                                                                               7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA 53
                                                               40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00194; TROPOMYÖSIN.
Complete proteome.
SEQUENCE 389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              389 AA
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EMBL; X74218; CABS0780.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; HISTONEH5.
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STRAIN=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
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MEDLINE=21145866; PubMed=11248100;
                                                                                                         44.0%;
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                                                                                     Query Match
Best Local Similarity 66.0%
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                                                               372 AA;
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                                         PRINTS, PI
SEQUENCE
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SEQUENCE FROM N.A.
STRAILLIZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R Varquez-Boland W., Schluer T., Simoes N., Tierrez A., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEVENTY 2937;
RAY M.C., Vianney A., Cotte-pattat N., Lazzarou. ...
RAY M.C., Vianney A., Cotte-pattat N., Lazzarou. ...
Characterization of the Erwinia chrysanthemi tol-pal ge
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ297885; CAC82708.1; SEOUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                   Science 294:849-852(2001).
BMBL; AL591981; CAD00019.1; -.
ListiList; LM001941; -.
InterPro; IPR002482; LysM.
Pfam; PR01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
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0.1-MAR-2002 (TrEMBLrel. 20, Created)
0.1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
0.1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 43.8%; Score 116.5; DB 16; Local Similarity 55.4%; Pred. No. 0.0026; les 31; Conservative 9; Mismatches 15;
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TOLA OR STM0747.
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Salmonella.
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SEQUENCE
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093946;
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Q8Z8C1;
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                                                                                                                                                                                            RESULT 7
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Couriney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Aterston R., Wilson R.K.,"
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLST: TO RIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

MEDLINE-21156231; PubMed-11258796;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Rannagara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sannagara S., Shiba T., Hattori M., Shinagawa H.; Sannagara S., Shiba T., Hattori M., Shinagawa H.; Bonomic Comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).

EMBL; AB005253; AAG55075.1; -

EMBL; AP002553; BAB34197.1; -

InterPro; IPR000104; Antifreeze 1.

PRINTS; PR00308; ANTIFREEZEI.
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MEDLINE=21074935; PubMed=11206551;
Perna N.T.; Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein, TolA).
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Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 113.5; DB 16; Length
49.3%; Pred. No. 0.0079;
ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAA----KKAEAKAYK-AAEAKKKAEA-----
                                                                                                                                                                                                                                                                                                                                 2534352116602D75 CRC64;
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InterPro, IPR000104, Antifreeze 1.
PRINTS, PR00308, ANTIFREEZEI.
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                                                                                                                                                                                                                                                                                                                                 407 AA; 41865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 49.3
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                            Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 AKAAADAKKKAEAEA 197
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Matches 33; Conserva
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Q8X965
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9

33; Conservative

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Kaiser B., Kunkel W., Saluz H.P., Munder T.;
"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ006637; CAA07165.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Doule L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKK---YAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                      157 EEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAALKKKAEAAEAAAAEARKKA 211
                                                                                                                                                                                                                                                                                                            Ascomycota; Saccharomycotina; Saccharomycetes;
26
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EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA----KYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.7%; Score 111; DB 3; Length 212; 55.9%; Pred. No. 0.0071; ive 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacularos
Saccharomycetales, mitosporic Saccharomycetales, Candida
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Last annotation update)
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Last annotation update)
                                                                                                                                            212 AA
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EMBL; AL627268; CAD05209.1; -.
Interpro; PR00104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                      Candida albicans (Yeast).
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                                                                                                                                            PRELIMINARY;
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les 33; Conserv
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SEQUENCE 376 AA:
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01-MAY-1999
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1454 AKKAEAARKAEAAKKAEAARKAEBAAKKAEBARKAEAAKKAEAARKAEBAKKAEBARKAEE 1513
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X MEDIINE=21681879; PubMed=11823852;

A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Arlat M., Edilault A., Brottier P., Camus J.C., Cattolico L.,

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

Signier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.,

I "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RESL, ALG46071; CAD16500.1;

RESL, ALG46071; CAD16500.1;

REPERPO, IPR003993; Treacle.

R InterPro; IRR03993; Treacle.

R PRINTS; PR01503; TREACLE.
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Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.8%; Score 100.5; DB 16; Length 53.7%; Pred. No. 0.058; ive 3; Mismatches 21; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin2055.
                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                 200 AA.
                                                                                                                                                                                                                                                                                   Created)
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STRAIN-CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                                                                                                                                                                                                                                                                                (TrEMBLrel. 20,
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                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                        RSC2793 OR RS00453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=305;
                                                                                                       1514 A 1514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA-----KYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites."; Mol. Bvol. 0:0-0(2002). EMBL, AV042083; AALIO508-11; -. SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
                                                    17;
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ch 41.5%; Score 110.5; DB 16; Length 376; 1 Similarity 53.5%; Pred. No. 0.014; 38; Conservative 5; Mismatches 11; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=YM,
MEDLINE=98115903; PubMed=9448114;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
Kappe S.H.I. Noe A.R. Fraser T.S., Blair P.L., Adams J.H.;
A family of chimeric erythrocyte binding proteins of malaria
parasites.";
Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
SEQUENCE 1701 AA; 199268 MW; EDA8EZDEFD87CE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.4%; Score 110; DB 5; Length 1701; 54.2%; Pred. No. 0.064; ive 5; Mismatches 14; Indels
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5855;
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Last annotation update)
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Michon P., Stevens J.R., Kaneko O., Adams J.H.;
                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1701 AA.
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MAEBL.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 55.77
Matches, 34; Conservative
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hes 32; Conservative
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                       Best_Local Similarity
Matches 38; Conserv
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NCBI_TaxID=73239;
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01-OCT-2000
  Query Match
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Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Sinces N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
EMBL, ALS6470; CAC97285.1; -.
ListList, LIN02055; -.
InterPro; IPR002482; LysM.
Hypothetical protein; Complete proteome.
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MEDLINE=20478054; PubMed=11021991;
Sun L. (Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20013326; PubMed=10544099; Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96187795; PubMed=8614977;
Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
"Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
positions 88 to 182.";
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
VCDI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 98.5; DB 16; Length 243; ilarity 50.0%; Pred. No. 0.1; Conservative 9; Mismatches 18; Indels 1;
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Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
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Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               KKYAKKEKAYAK-----KAEKAAKKAEAKAYKAAEAKK----KAEAKYKAEAAKAAAK 50
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                                                                                                                                                                                                                                                                                           Length 311;
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NCBL_TaxID=31273;
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                                                                                                                                                                                                                                                                                                                                             Indels
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                   Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL, U42580; AAC96576.1; -.
InterPro; IPR002048; FF-hand.
PROSITE; PS00018; FF-hand.
SEQUENCE 311 AA; 35390 MW; 9780E9582AFEF88A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                      37.0%; Score 98.5; DB 12;
43.9%; Pred. No. 0.13;
ive 8; Mismatches 18;
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nes 29; Conservative
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SEQUENCE FROM N.A.

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WEDLINE=20063166, PubMed=10594009;

WEDLINE=20063166, PubMed=10594009;

MEDLINE=20063166, PubMed=10594009;

MEDLINE=20063166, PubMed=10594009;

MEDLINE=2011, Resident of the sequence of the 
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
WCBI_TaxID=5191;
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36.1%; Score 96; DB 3; Length 213;
Best Local Similarity 44.8%; Pred. No. 0.15;
Matches 30; Conservative 4; Mismatches 17; Indels
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16; Gaps

94 KLAKKEKAAAAPKKPAAKKAAAPKKDAAPKKAAAPKKAAAAPKSAAAKKKLLDAKKAAAKK 153

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3 KYAKKEKAYAKKAEKAAKKA------EAKAYKAAEAKKKAEAKYKAEAAK 46

Search completed: March 10, 2003, 12:25:55 Job time : 30.654 secs

|||:|| 154 PARKAA 160 47 AAAKEAA 53

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:15:01; Search time 29.1814 Seconds (without alignments) 255.712 Million cell updates/sec

US-09-816-989A-3 266 score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 101002:\*

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| SIDSS/gcgdata/geneseqg-embl/AA1980.DAT:\*
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# SUMMARIES

	Description	Copolymer molecula	Listeria monocytog	Recombinant copoly	Copolymer molecula	Peptide #10 used i					
	ID	AAY82573	AAY82575	AAY82576	AAY82574	AAY82577	AAY82572	ABB49123	AAR06446	AAY82571	AAY98499
	DB	21	21	21	21	21	21	23	11	21	23
	Query Match Length DB		77	86	99	109	45	239	106	35	100
de	Query	100.0	92.3	87.6	74.4	67.9	50.6	43.8	41.7	39.3	39.1
	Score	266	245.5	233	198	180.5	134.5	116.5	111	104.5	104
	Result No.	1	7	e	4	2	9	7	∞	6	10

Amino acid polymer Poly-Lys-Ala used Nucleic acid trans Recombinant copoly	Anno acid sequenc Human protein sequ Plasmodium yoelii C albicans apoptos Mycobacterium bovi	M. tuberculosis hi M. tuberculosis hi Zuotin. Saccharom Human zuotin prote S cerevisiae apopt	Herbicidally activ Nucleic acid (NA) Trypanosoma cruzi Trypanosoma cruzi Trypanosoma cruzi	Neisseria IgA-Prot Novel human diagno High affinity macr Human DNA modifica Human protein sequ Human protein sequ	Drosophila melanog Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Synthetic helical PspC alpha-helix c	Streptococcus pneu S. pneumoniae PspC Quail H1 histone p Human ORFX protein
			23 ABB93466 18 AAW24449 16 AAR84568 116 AAR84569 16 AAR84569	∢		18 AAW14593 20 AAY43384 21 AAY76981 23 ABP00299
1000		214 433 433 433		334 334 46 279 198		929 929 219 111
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104	103 101 101 97.5	9 9 9 4 4 6 9 9 9 9 7 7 4 4 4	94 93.5 91.5 91.5	88 88 89 9.50 89 9.50 89 9.50 89 9.50	88.5 87.5 87.5 87.5 85.5	85.5 85.5 84.5
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# ALIGNMENTS

AAY82573 standard; peptide; 56 AA RESULT 1 AAY82573

AAY82573;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

glatizamer acctate; autojament disease; antiarthitic; neuroprotective; osteopathic; immunosuppressive; antithyroid, antiinflammatory; antidatelic; thyromimeletic; haemostatic; antibaoriatic; dermatory; antidatelic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; (Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US22402 24-SEP-1999; 

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

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ANYB2571 to AAYB2577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight copolymer. The polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or retributed diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple steleorists, rheumarcing arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, contact sensitivity disease, diabetes mellitus, Graves disease, Gillain-Barre's syndrome, Hashimoro's disease, alidopathic myxoedema, myasthenia gravis, psyndrome, Hashimoro's disease, and delated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delated-mediated diseases which are analogous to molecular weights and physical properties which are analogous to molecular weights melecules, which makes them ideal for use as
                                                                                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular weight, markers.
                                                                              WPI; 2000-317499/27.
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                            Gad A,
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Gaps ö 100.0%; Score 266; DB 21; Length 56; 100.0%; Pred. No. 3e-20; ive 0; Mismatches 0; Indels Local Similarity 100. Query Match Matches

RESULT 2

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AAY82575 standard; peptide; 77 AA.

AAY82575;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antidityroid; antiinflammatory; antidiabetic; thyromimetic; hemostatic, antipsoriatic; dermatological; antianaemic; immunosuppressive, demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. 

WO200018794-A1.

06-APR-2000.

99WO-US22402. 24-SEP-1999;

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. (TEVA-)

Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular convention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing inmune diseases in a mammal. Autoimmune conditions, antibody-mediated diseases and inflammatory conditions, e.g. multiple antibody-mediated diseases and inflammatory conditions, e.g. multiple cancering also acophoritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia cuveoretinitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves CC disease, Guillain-Barres s syndrome, Hashimoto's disease, and myasthenia gravis, psoriated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delined molecular weights and physical properties which are analogous to glatinamer acetate molecules, which makes them ideal for use as nolecular weight markers.

77 AA; Sequence

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0; Indels 21; Gaps 92.3%; Score 245.5; DB 21; Length 77; 72.7%; Pred. No. 4.9e-18; ive 0; Mismatches 0; Indels 21; 56; Conservative Similarity Query Match Best Local 9 Matches

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40 YKAEAAKAAAKEAAYEA 56 ઠે

61 YKAEAAKAAKEAAYEA 77

AAY82576 standard; peptide; 86 AA. AAY82576

28-JUL-2000 (first entry) AAY82576;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

glatitamer accate; autoimmune disease, antiarthritic; neuroprotective, osteopathic; immunosuppressive, antichyroid; antificammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; dulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer; molecular weight marker; TV-marker; immune disease; 

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a composition corresponding to the copolymer. The polypeptides may also be used for treating and terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, clemyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Ginllain-Barre's syndrome, Hashimoto's disease, idiopathic mycoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hyperesnositivity. The polypeptides of the invention have defined molecular weights and physpetides of them are analogous to
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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 pemphigus vulgaris; systemic lupus erythematosus.
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Pred. No. 1e-16;
2; Mismatches
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TEVA PHARM USA INC.
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight con and an amino acid composition corresponding to the copolymer. The copolymer invention are used as molecular weight markers for glatizamer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple scleenyelinating diseases. Such diseases incliment haemolytic anaemia, autoimmune ophoritis, osteoarthritis, autoimmune haemolytic unecerimitis, Crohn's disease, chonic immune thyroiditis, autoimmune uvecreinitis, crohn's disease, chonic immune thyroiditis, autoimmune uvecreinitis, crohn's disease, habinoto's disease, idiopathic myxoedema, myasthenia gravis, psentiasis, pemphigus vulgaris, or systemic illust erythematosus Mediated mediated diseases which can be treated include the contact sensitivity disease, diabetes mediated myasthemic collinations are madiated mediated diseases which can be treated include the contact sensitivity disease, diabetes mediated myasthemic collinations are mystemic contact sensitivity disease, diabetes mediated collinations and contact sensitivity disease, diabetes mediated collinations and collinations and collinations and collinations are demonstrated myxoedema, myasthemic sensitivity diseases which can be treated collinations and collinations and collinations and collinations and collinations and collinations and collinations are collinated mysthemic collinations and collinati
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                     glatiamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antihyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatory antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     include host-versus-graft disease, graft-versus-host disease, and delayed-vype hypersensitivity. The polypeptides of the invention defined molecular weights and physical proporties which are analoglatinamer acetate molecules, which makes them ideal for use as
Copolymer, molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 198; DB 21;
80.3%; Pred. No. 2.6e-13;
ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US22402.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   WO200018794-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1998;
                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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EAAYEA 66

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RESULT 5

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hacmolytic ansemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune thrombocytopaenia uveoretinits, crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus Graves disease, myasthenia gravis, psyndrome, Hashimoto's disease, allique erythematosus. Mediated-mediated disease, which can be treated include host-versus-graft disease, graft-versus-short disease, and colletined molecular weights and phypeptides of the invention have defined molecular weights and phypatical properties which are analogous to molecular weights molecules, which makes them ideal for use as along the molecular weights molecules which markes them ideal for use as
                                                                                                                                                                                                                                   optoprime, morrous market, include the morror of a distribution to the morror of antidabetic; immunosuppressive; antichyroid; antidabetic; thyromientic; heamediatic; antipacoriatic; dermaclogical; antidanaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crowing sissease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; dullain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ,ID NO:7.
                                                                                                                                                                                                                      Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                        pemphigus vulgaris; systemic lupus erythematosus.
                        AAY82577 standard; peptide; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English
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USA INC.
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                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1998;
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                                                                                                                       28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000.
                                                                     AAY82577;
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AAY82577
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight end ocid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treated include either cell-mediated or antibody-mediated diseases and inflammacry conditions, e.g. multiple antibody-mediated diseases and inflammacry conditions, e.g. multiple canemia, autoimmune ophoritis, osteoarthritis, autoimmune haemolytic sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune baemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia cuecerinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barrer's syndrome, Hashimoto's disease, diabetes mellitus, contact sensitivity disease, diabetes mellitus, crastemic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated meledated diseases which can be treated deliaped-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                             glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antibhyroid; antiinflammatory; osteopathic; immunosuppressive; antibhyroid; antiinflammatory; dermatory; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                             AAY82572 standard; peptide; 45 AA.
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                                                                                                                                                                                                                                                                                                                     28-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
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3;

Gaps

1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK------39

67.9%; Score 180.5; DB 21; Length 109; 45.9%; Pred. No. 2.6e-11; tive 3; Mismatches 3; IndelB 53;

Query Match 67.9 Best Local Similarity 45.9 Matches 50; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to hosynthesis and biodegradation, especially biosynthesis of vitemain B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pot_sequences.
                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Chakrabit A, Durant L; Perez-Diaz J, Baquer F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, pe Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                               Gaps
                                                                                                                                                                                                                                                                                                          Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                 5; Indels 13;
                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA
                                                  Score 134.5; DB 21; Length 45;
Pred. No. 4.7e-07;
0; Mismatches 5; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID No 1828; 192pp; French.
                                                                                                                                                                                                                                                                                  Listeria monocytogenes protein #1827.
                                                                                                                                                                                                 ABB49123 standard; Protein; 239 AA
                                                  Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                     05-FEB-2002 (first entry)
 molecular weight markers
                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
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                          45 AA;
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                                                                                                                                                                                                                                                                                                                                                                            WO200177335-A2
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                                                                                                                                                                                                                            ABB49123;
                          Sequence
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                                                                                                              Gaps
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The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also,
                                                                                                                                                                                                     1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in contain aning acids.
                                                                                                              ;
                                                     DB 23; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.7%; Score 111; DB 11; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing genes encoding random polymers of aminoacid(s) - i
producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                           Indels
                                                                                                              15;
                                               Score 116.5; DB 2. Pred. No. 0.00018; 9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                      AAR06446 standard; protein; 106 AA.
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                                               43.8%;
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                                                                                Local Similarity 55.4 nes 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis;
239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAR06446;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular response to a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, didopathic myxoedema, myasthenia gravis, psyndrome, Hashimoto's disease, didopathic myxoedema, myasthenia gravis, peemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory antiantamic; immunosuppressive; hemostatic; antipocriatic; dermacological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; politis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                     Gaps
                                                                           1 AKKYAKKEKAYAKKAEKAAKKAE------AKAYKAAEAKKKAEAKYKAEAAKA 47
                                                                                                     14;
Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pemphigus vulgaris; systemic lupus erythematosus.
                                 6; Mismatches
                                                                                                                                                                                                                                                                                                              AAY82571 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
           47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US22402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0101693
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-317499/27
             Best Local Similarity
                                                                                                                                                              AAK-EAAYE 55
                                                                                                                                                                                       | | :|||:
AEKAKAAYK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200018794-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000
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                                 Matches
                                                                                                                                                            48
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nucleic acid to a coll. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for desting. Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                  2,
                delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a transporter system for delivering
graft-versus-host disease, and
                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                                                                                                                                                                  21;
                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                DB 21; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #10 used in nucleic acid transporter system.
                                                                                                                                              39.3%; Score 104.5; DB 21; 51.8%; Pred. No. 0.00039; iive 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 125-128; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                  AAY98499 standard; Peptide; 100 AA.
 include host-versus-graft disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0167641.
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93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                 Local Similarity 51.8
tes 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-281993/24.
                                                                                                             35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6033884-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                    AAY98499;
                                                                                                                                                Query Match
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                            RESULT 1(
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100 AA;

Seguence

degradation.

Length 100;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
3..100
/note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease;
                                                                                                                                  23
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                                                                                                                              1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA
      Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith LC;
                                                                    17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparrow J,
      Score 104; DB 21
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid polymer seq ID NO: 64 of US5994109.
                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 123-124; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gottchalk S,
                                                                                                                                                                                                                                                                                                                                               AAY59044 standard; peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid delivery; cancer
      39.1%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0167641.
92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-038262/03.
Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                AAY59044;
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AAY 59044

AAY 59044

AAY 59044

AAY 50 7-b AAY 50 7-b
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100 AA;

Sequence

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                                                                                                                                                                                                                                                                            spacer molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                              /note= "Lys-Ala in positions 3-100 may be present absent"
                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
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                                                           1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sparrow J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.1%; Score 104; DB 22; Length 100; 58.2%; Pred. No. 0.0013; ive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                            Nucleic acid transport; cytosis; ligand; lysis agent; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                Poly-Lys-Ala used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottchalk S,
Score 104; DB 21
Pred. No. 0.0013;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 131; 111pp; English
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cristiano RJ,
                                                                                                                                                            AAU04289 standard; Peptide; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0167641.
92US-0855389.
93WO-US02725.
39.1%;
llarity 58.2%;
Conservative
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-365933/38
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA;
                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                             US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993;
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19-MAR-1993;
 Query Match
Best Local Simi
Matches 32;
                                                                                                                                                                                                                    23-OCT-2001
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                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                        AAU04289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Matches
                                                                                                                                RESULT 12
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RESULT 13 AAB45852

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To improve the expression of rCOP-1 polypeptides in B. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US(469100), MRLB B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences. The cop-1 polypeptide may be cleaved from the fusion protein. The COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, BEL KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. They are used to prevent, arrest or control a encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AEAAAEAEKAKYKKKAKEAEYKKKAKAAAEAEYKKEAEEAEYKKYKKKAKKAKKAKKAKE 122
                                                             Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
                       Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKA-YAKKAEKAAKKAEAKAYKAAEAKKKAE----
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Pred. No. 0.0026;
7; Mismatches 1
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                                                                                                                                                                                                                                                                                            90EP-0301700
                                                                                                                                                                                                                                                                                                                                         90US-0473845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              (REPL-) REPLIGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-255848/34.
                                                                                                               multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also AAQ05665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ05664
                                                                                                                                                                                                                                                                                              16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                         07-FEB-1990;
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                                                                                                                                                                                                                                                    22-AUG-1990.
                                                                                                                                                                                                       EP383620-A.
                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, applipproteins, receptors, drugs, oncogenes, tunor antigens, tunor
                                                                                                                                                                                                                       Nucleic acid delivery, nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel system (I) for delivering a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
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                                                                                                                                                                               Nucleic acid transporter system peptide ligand SEQ ID NO 64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 125-126; 105pp; English
                                          AAB45852 standard; Protein; 100 AA
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92US-0855389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 58.2
1es 32; Conservative
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                                                                                                                                                                                                                                                                                                                                         Unidentified
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20-MAR-1992;
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                                                                                       AAB45852;
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13; Indels 24; Gaps

Matches

8

11; Length 154;

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The invention provides heat-killed Mycobacterium vaccae, or recombinant

M. vaccae proteins. The M. vaccae proteins may be employed to activate

T cells and natural killer cells, to stimulate the production of

cytokines, to enhance the expression of co-stimulatory molecules on

dendritic cells and monocytes, and to enhance dendritic cell maturation

and function. The proteins can be expressed by standard recombinant

and function. The proteins can be expressed by standard recombinant

and function, and detection comprising the proteins or

nucleic acid sequences encoding the proteins can be used for the

treatment, prevention, and detection of disorders including infectious

treatment are used for treatment of diseases of the respiratory system,

such as mycobacterial infections, asthma, allergies, tuberculosis,

such as mycobacterial infections, asthma, allergies of the skin such as

psoriasis, atopic dermatitis, ecreme, allergic contact dermatitis,

alopecia areata, and skin cancers such as basal carcinoma, squamous cell
                                  Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma.
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Best Local Similarity 55.0%; Pred. No. 0.0038;
Matches 33; Conservative 3; Mismatches 18; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tan P, Visser ES, Watson J;
Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing immune response to an antigen
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97US-0996624.
97US-0997080.
97US-0997362.
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                                                                                                                                                                          Mycobacterium vaccae.
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N-PSDB; AAZ11393.
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Search completed: March 10, 2003, 12:21:29 Job time : 30.1814 secs

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Page

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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:26:10 ; Search time 16.6582 Seconds (without alignments) 141.764 Million cell updates/sec

US-09-816-989A-3 266 Title: Perfect score:

1 AKKYAKKEKAYAKKAEKAAK.......BAKYKAEAAKAAAKEAAYEA Sequence:

56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188354 seqs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

1: \cgn2 \( \) \cgn \( \)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
1	266	100.0	56	10	US-09-816-989A-3	Segmence 3, Appli
7	245.5	92.3	77	10	US-09-816-989A-5	
ю	233	87.6	98	10	US-09-816-989A-6	9
4	198	74.4	99	10	US-09-816-989A-4	Sequence 4, Appli
S	180.5	67.9	109	10	US-09-816-989A-7	
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80	104.5	39.3	35	10	US-09-816-989A-1	
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10	96.5	36.3	452	σ	US-10-184-832-5	Sequence 5, Appli
11	89.5	33.6	356	σ	US-09-820-843A-27	
12	82.5	31.0	369	δ	US-09-820-843A-95	
13	82	30.8	619	σ	US-09-882-774-1	
14	82	30.8	892	10	US-09-815-242-13765	Sequence 13765, A
15	81	30.5	890	10	US-09-815-242-10314	Sequence 10314, A
16	80.5	30.3	309	σ	US-09-820-843A-24	Sequence 24, Appl
17	80.5	30.3	617	10	US-09-864-761-36182	Sequence 36182, A
18	79	29.7	582	10	US-09-919-497-100	Sequence 100, App
19	78	29.3	218	σ	US-09-999-724-48	Sequence 48, Appl

Sequence 5854, Ap Sequence 5, Appli Sequence 37061, A Sequence 7, Appli Sequence 17, Appli Sequence 6, Appli Sequence 9, Appli Sequence 11, Appli Sequence 8, Appli Sequence 8, Appli Sequence 3, Appli Sequence 3, Appli Sequence 127, Appli Sequence 127, Appli Sequence 127, Appli Sequence 128, Appli Sequence 129, Appli Sequence 139, Appli Appli Sequence 139, Appli	Sequence 131, App Sequence 213, App Sequence 4122, Ap Sequence 53, Appl Sequence 51, Appl Sequence 5198, Ap
US-09-738-626-5854 US-10-093-892-5 US-10-093-892-5 US-09-999-724-90 US-10-093-892-7 US-10-093-892-7 US-10-093-892-9 US-10-093-828-11 US-09-993-724-8 US-09-993-724-8 US-09-983-428-8 US-09-984-761-35241 US-09-864-761-35241	0 US-09-805-301-131 (10 US-09-764-846-233 (10 US-09-738-626-4122 (10 US-09-883-825-53 (10 US-09-883-825-51 (10 US-09-815-242-5198 (10 US-09-764-846-242
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# ALIGNMENTS

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JUNEAU SEQUENCE 3, Application US/09816989A

Fatent No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COOLUMER I RELATED POLYBEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT FILING DATE: 2001-03-23

PRIOR PAPLICATION NUMBER: PCT/US99/22402

PRIOR PAPLICATION NUMBER: PCT/US99/22402

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 3

LENGTH: 56

LENGTH: 56
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ORGANISM: Artificial Sequence
US-09-816-989A-3
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56 Sequence 5, Application US/09816989A Patent No. US20020115103A1 , GENERAL INFORMATION: , APPLICANT: Gad, Alexander , APPLICANT: Lis, Doris US-09-816-989A-5 8 셤

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-P-CT-US CURRENT PRILING DATE: 2001.03-23 PRIOR PLING DATE: 2001.03-23 PRIOR PLING DATE: 1999-09-25 PRIOR FILING DATE: 1999-09-25 PRIOR FILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7 SEQ ID NOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.3%; Score 245.5; DB 10; Length 77; Best Local Similarity 72.7%; Pred. No. 5.3e-18; Matches 56; Conservative 0; Mismatches 0; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK------
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87.6%; Score 233; DB 10;
Best Local Similarity 62.8%; Pred. No. 9.9e-17;
Matches 54; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/09816989A; Patent No. US20020115103A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YKAEAAKAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-816-989A-6
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US-09-816-989A-4
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Sequence No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23
PRIOR PAPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1999-09-25
PRIOR PELING DATE: 1999-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAEKAYAKKAKAAKAKEKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- YKAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 180.5; DB 1
Pred. No. 1.7e-11;
3; Mismatches 3
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Pred. No. 2e-13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERBENCE: 2609/6007-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VON THE SEQ ID NOS: 7
SOFTWARE: PATENTIN VON SET 1000 NOS: 7
SOFTWARE: PATENTIN VON SET 1000 NOS: 7
SOFTWARE: PATENTIN VON SET 1000 NOS: 7
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4, Application US/09816989A
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Best Local Similarity 45.9%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 80.3%;
Matches 53; Conservative
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Sequence 201, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: Methods using Mycobacterium Vaccae

TITLE OF INVENTION: OF Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: OF Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: OF Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: OF IMMUNOSCA

TITLE OF INVENTION: 2002-01-18

FILE REFRENCE: 1990-17

PRIOR PILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SOUTHARE: PASESEQ for Windows Version 3.0

LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.3%; Score 104.5; DB 10; Best Local Similarity 51.8%; Pred. No. 0.00015; Matches 29; Conservative 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 38.7%; Score 103; DB 9; 1 Similarity 55.0%; Pred. No. 0.0014; 33; Conservative 3; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                                                                                                           APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A.-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHIAN OF SEQ ID NOS: 7
SOFTWARE: PARCHIAN VERSION 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09820843A
Publication No. US20030039963A1
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICAT: Council of Scientific and Industrial Research
TITLE OF INVERTION:
TITLE OF INVERTION: USFUL AS ANTI-INFECTIVES
TITLE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

39.7%; Score 105.5; DB 9; Length 372;
Best Local Similarity 48.2%; Pred. No. 0.0013;
Matches 27; Conservative 14; Mismatches 14; Indels 1
                 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc_feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 134.5; DB 10;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                     ; Sequence 2, Application US/09816989A
; Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-820-843A-8
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US-09-816-989A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AKKEKAY--AKKAEKAAKKAEAKAYKAABAKKKAEAKY----KABAAKAAAKEAAYE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
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                                                                                                                                                                                                                                                                                                                     Length 369;
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45.6%; Pred. No. 0.45;
tive 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 EKAYAKKAEKAAKK--AEAKAYKAAEAKKK-AEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oblem, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hodges, Robert
TITLE OF INVENTION: Use of Coiled-Coil Structural SC
TITLE OF INVENTION: Use of Coiled-Coil Structural
TITLE OF INVENTION: Structure-Specific Peptides
FILE REFERENCE: 003592-007
CURRENT APPLICATION NUMBER: US/09/882,774
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 16
                                                                              NAME/KEY: misc_feature;
CTHER INFORMATION: conserved hypothetical protein;
NAME/KEY: misc_feature
CTHER INFORMATION: gi|3322751
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                             Query Match 31.0%; Score 82.5; DB 9;
Best Local Similarity 44.2%; Pred. No. 0.24;
Matches 23; Conservative 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13765, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR ELLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-882-774-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09882774; Publication No. US20030021795A1; GENERAL INFORMATION: APPLICANT: Houston, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.8
Best Local Similarity 45.6
Matches 26; Conservative
           ORGANISM: T. pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-815-242-13765
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US-09-882-774-1
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Publication No. US20030039963A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/09820843A
Publication Wo. US20030039963A1
Publication Wo. US20030039963A1
Publication Wo. US20030039963A1
APPLICANT: Council of Scientific and Industrial Research
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARR: PEtentin Version 3.0
SOFTWARR: PEtentin Version 3.0
LENGTÉ: 369
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REFERENCE: MPI2001-0656P1NM
CURRENT APPLICATION NUMBER: 05/10/184,832
CURRENT FILING DATE: 2002-06-28
PRIOR PILIATION NUMBER: 60/303,250
PRIOR PILIATION NUMBER: 60/303,250
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASLERQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.3%; Score 96.5; DB 9; Length 452; 55.1%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.5; DB 9; Length 3:
Pred. No. 0.047;
6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAKAAAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
COTHER INFORMATION: tolA protein
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9656364
US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6%;
Best Local Similarity 48.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 55.1
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
US-10-184-832-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-820-843A-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA--KYKAEAAKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.8%; Score 82; DB 10; Length 892; Best Local Similarity 38.2%; Pred. No. 0.65; Matches 21; Conservative 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%; Score 81; DB 10; Length 890; 33.3%; Pred. No. 0.82; tive 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Obleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: WH. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FRIOR APPLICATION NUMBER: 60/242,578
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2001-02-16
SOFTWARE: FAST SEQ ID NOS: 14110
SOFTWARE: FAST SEQ ID NOS: 14110
SEQ ID NO 13765
TYPE: PROTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-25
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
LENGTH: 990
LENGTH: 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
COCATION: (1)...(892)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10314, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.33
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-815-242-10314
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Sequence 4, Sequence 4, Sequence 2, Sequence 2, Sequence 3, Sequence 3, Sequence 3,

Sequence

Sequence 2, Sequence 2, Sequence 2, Sequence 2,

Perfect score:

Run on:

Sequence:

Scoring table:

Database

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DB 4; Length 56;
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FLING DATE: 18-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FLING DATE: 18-DEC-1996
ATTORNEY/AGENT INPOMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INPOMBER: 33,064
REGISTRATION NUMBER: 33,064
REGISTRATION INPORMATION:
NAME: SUllivan, Sally A.
REGISTRATION INPORMATION:
TELEPHONE: 303-499-8080
                                                                                              US-08-214-222-4
US-08-467-852A-5
US-08-467-491A-5
US-08-247-491A-5
US-08-214-164-2
US-08-214-164-2
US-08-246-852A-3
US-08-247-491A-3
US-08-246-652A-3
US-08-247-491A-3
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I: 5370 Manhattan Circle, Suite 201
Boulder
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                                                                                                                                                                                                                                                                                                                                                          -08-468-985-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.1%; Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08991008A
Patent No. 615396
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Petros, John A.
APPLICANT: Rarr, Joan F.
APPLICANT: Rarr, Joan F.
APPLICANT: Rarr, Joan F.
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Pollycationic Ol
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and S
STREET: 5370 Manhattan Circle, Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: no
; ANTI-SENSE: NO
US-08-993-008A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CO
COUNTRY: US
ZIP: 80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-993-008A-6
  Query Match
  4, Appl

10. Appl

10. Appli

10.
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Sequence 13, Appl
Sequence 2, Appli
Sequence 16, Appl
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, App.
                                                                                                                                                                     March 10, 2003, 12:15:04 ; Search time 9.92405 Seconds (without alignments) 166.029 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64,
Sequence 201,
Sequence 201,
Sequence 5, A
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Sequence 10,
Sequence 10,
Sequence 2,
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Patent No. 5
                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAK.......EAKYKAEAAKAAAKEAAYEA 56
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Sequence 6
Sequence 6
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Sequence
Sequence
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Sequence 8
Sequence 8
Sequence 1
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/cgm2 6/ptcdate/2/laa/6A COMB.pep:*
/cgm2 6/ptcdata/2/laa/6B COMB.pep:*
/cgm2 6/ptcdata/2/laa/epcTUS COMB.pep:*
/cgm2 6/ptcdata/2/laa/pcTUS COMB.pep:*
                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-993-008A-6
US-08-460-991A-64
US-08-460-911A-64
US-08-460-911A-64
US-09-95-855-201
US-09-95-855-201
US-09-929-329-5
US-08-929-329-5
US-08-929-329-5
US-08-929-329-5
US-08-929-329-8
US-08-94-849-1
US-08-216-894-8
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US-08-216-894-16
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US-08-216-894-16
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US-08-216-894-10
US-08-216-894-2
US-09-115-746-10
US-09-115-746-10
US-09-115-746-10
US-08-216-894-2
US-09-115-746-10
US-08-216-894-2
US-09-115-746-10
US-08-216-894-2
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US-08-436-703B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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266
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Match Length
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103 101 99.5 94.5

Result No.

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.1%; Score 104; DB 3; Length 100; Best Local Similarity 58.2%; Pred. No. 0.0004; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                     GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Lys Ala" in positions 3 to 100 may present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTENG FOR Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                       Sequence 64, Application US/08167641C
Patent No. 6033884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08460971A
Patent No. 6150168
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 205/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
COTHER INFORMATION:
US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                     US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-460-971A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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                              Gaps
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                              5
                                                                                                      1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.1%; Score 104; DB 2; Length 100; Best Local Similarity 58.2%; Pred. No. 0.0004; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Getchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
Best Local Similarity 58.2%; Pred. No. 0.00022; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: 18M Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                                Sequence 64, Application US/08460890A
Patent No. 5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEZ: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                               RESULT 2
US-08-460-890A-64
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Sequence 201, Application US/09095855

Sequence 201, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:
APPLICANT: Tan. Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Compounds and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.1%; Score 104; DB 4; Length 100; 58.2%; Pred. No. 0.0004; tive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle STATE: WA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: WA MEDIUM TYPE: Diskette
                                                                                                                                                                                                                             MEDIUM TYPE: storage
COMPUTER: IBM COMPALIAL
OPERATING TOWN THEN EN COMPALIAL
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASISEQ for Windows 2.0
CUMERNY PAPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
GIASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/859,389
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,2078
FILENCOMMUNICATION INFORMATION:
TELEPONE: (213) 555-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
FUNCTH: 100 amino acids
                                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.23
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-095-855-201
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Patent No. 6177554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
MUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
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39.1%; Score 104; DB 4; Length 100;
Best Local Similarity 58.2%; Pred. No. 0.0004;
Matches 32; Conservative 4; Mismatches 17; Indels
                     TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1.995
FILING DATE: March 10, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 10, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 10, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION
                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Gottchalk, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-462-040-64
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1 AKKYAKKEKAY--AKKAE-----KAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAK
                                                                                                                                                                            APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Dalton, John P
APPLICANT: Kappe, Stefan
ITTLE OF INVENTION: Plasmodium Proteins Useful for Preparing
TITLE OF INVENTION: Vaccine Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/929,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 3;
Pred. No. 0.013;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lite.

Petros, John.

1: Wey, Shlow-Jyl

T: Karr, Joan F.

NT: Pohl, Jan

NT: Pohl, Jan

Polycationic Oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08993008A Patent No. 6153596
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Barnes & Thornburg STREET: 11 S Meridian CITY: Indianapolis STATE: Indiana
                                                                                                            Sequence 5, Application US/08929329
Patent No. 6120770
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGIGTRATION NUMBER: 38,833
REFRENCE/DOCKET NUMBER: 9359:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-745
TELEPRA: (317) 231-745
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liotta, Dennis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 38.0%;
1 Similarity 51.7%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POINT NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: Greenlee,
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: ""'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Liotta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                       US-08-929-329-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-929-329-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAK---AYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-205-426-201

Sequence 201, Application US/09205426

j Pattent No. 64066704

GENERAL INFORMATION:
APPLICANT: Tan. Paul L. J.
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
CURRENT FILING DATE: 11900.10024

CURRENT FILING DATE: 1998-12-04

EARLIER PILING DATE: 1998-06-11

EARLIER PILING DATE: 1999-12-23

EARLIER PILING DATE: 1997-06-12

EARLIER PILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-13

NUMBER OF SEQ 1D NOS: 208

SOFTWARE FASTERE FILING DATE: 1996-08-29

NUMBER OF SEQ 1D NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.7%; Score 103; DB 4; Length 223; Best Local Similarity 55.0%; Pred. No. 0.0011; Matches 33; Conservative 3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.7%; Score 103; DB 4; Length 223; Best Local Similarity 55.0%; Pred. No. 0.0011; Matches 33; Conservative 3; Mismatches 18; Indels
OPERATING SYSTEM: DOS
SUFTWARE: FastSEQ for Windows Version 2.0
SUGRENT APPLICATION DAY:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-ANG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 201: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Mycobacterium vaccae US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 201
LENGTH: 223
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Gaps
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Tood
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AKKVAK--KAPAKKATKAAKKAATKA-PARKAATKAPAK-KA-ATKAPAKKA 157
                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 35.5%; Score 94.5; DB 3; Length 214; Best Local Similarity 63.5%; Pred. No. 0.0078; Matches 33; Conservative 2; Mismatches 12; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.3%; Score 94; DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
       FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cahryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NS-08-346-849-2

VS-08-346-849-2

; Sequence 2, Application US/08346849

· Patent No. 5670483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brook, David E.
REGISTRATION NUMBER: 22,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-346-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4%; Score 99.5; DB 4; Length 48; 58.3%; Pred. No. 0.00052; tive 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KEKAYAKKAEKAAKKAEAKAYKAABAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09041889;
Sequence 27, Application US/09041889;
Fatch No. 603364;
SENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cheav, Offer
TITLE OF INVENTION: Ulcerative Colitis, and Clinic, TITLE OF INVENTION: Ulcerative Colitis, and Clinic, TITLE OF INVENTION: Ulcerative Colitis, and Clinic, TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STRATE: California
COUNTRY: USA
                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
RPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/POCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
: 5370 Manhattan Circle, Suite 201
Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 303-499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-08-993-008A-5
                                                                                   as
                                   CITY: BOU
STATE: CO
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                            CITY: Washington, D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-216-894-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-115-746-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 A 53
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APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Lockehin, Cuttis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                2 KKYAKKEKAYAKKAEKAAKK--AEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                            2 KKYAKKEKAYAKKAEKAAKK--AEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08216894

Patent No. 5876734

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Otsu, Keiko

ITILE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.3%; Score 94; DB 2; Length 433; Best Local Similarity 47.4%; Pred. No. 0.018; Matches 27; Conservative 7; Mismatches 21; Indels
Best Local Similarity 47.4%; Pred. No. 0.018;
Matches 27; Conservative 7; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,284A

FILING DATE: 22-AUG-1994

CLASSIFICATION NUMBER: 07/973,326

RIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,326

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: BROOK, DAYIG E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: MIT-6008A

TELECOMMUNICATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08293284A
Patent No. 5955343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 433 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-216-894-8
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYK-----AEAAKAAAKEA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIAGNOSING INFECTION CRUZI
                                                                                                                    COUNTRY: USA

ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
    APPLICANT: Kirchhoff, Louis V.
    APPLICANT: Otsu, Kelko
    TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNO, TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
    NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Foley & Lardner
    STREET: 3000 K Street, N.W., Suite 500
    COUNTRY: Washington, D.C.
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
FOLGY, E Lardner
STREET: 3000 K Street, N.W., Suite 500
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us-09-816-989a-3.open.rai

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APPLICANT: Abang, Shuguang
APPLICANT: Lockshin, Curris
APPLICANT: Lockshin, Curris
APPLICANT: High, Alexander
APPLICANT: High States
ITILE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
ITILE OF INVENTION: THEREOR
NUMBER OF SEQUENCES: A ADDRESS:
ADDRESSEE: HAMILTON: THEREOR
NUMBER OF SEQUENCES: A ADDRESS:
ADDRESSEE: HAMILTON: ROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Two Militia Drive
CITY: Lexington
STREET: Pro Militia Drive
CITY: Lexington
STREET: Pacentine Release #1.0, Version #1.25
COMPUTER: READABLE FORM:
MEDIUTATION NUMBER: US/08/346,849
FILING DATE: 20 DECEMBER 1992
ATTORNEY APPLICATION NUMBER: 22.532
REFERENCE/DOCKET NUMBER: 22.532
REFERENCE/DOCKET NUMBER: MIT-6008
TELEBRONE (617) 861-6540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 and naino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Anno acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYK-----AEAAKAAAKEA 52
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.8%; Score 92.5; DB 4; Length 643; Best Local Similarity 47.5%; Pred. No. 0.039; Matches 29; Conservative 6; Mismatches 15; Indels 11;
HAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5300
TELEFAX: (202)672-539
TELEFAX: (403)6
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: TYPE: protein
US-09-115-746-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-346-849-16
; Sequence 16, Application US/08346849
; Patent No. 5670483...
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US-08-346-849-16
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Gaps
                                               Ξ;
34.4%; Score 91.5; DB 1; Length 60; 52.0%; Pred. No. 0.0041; tive 4; Mismatches 19; Indels
                                                                                            2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAEAKYKAEAAKAAAK 50
Query Match
Best Local Similarity 52.09
Matches 26; Conservative
```

1;

1 KAAAKRKAALAKKKAAAAKRAAKKAKKKKKAAKKKKAAKKKPAKKSPKK 50

Search completed: March 10, 2003, 12:30:02 Job time: 9.92405 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:04; Search time 19.3544 Seconds (without alignments) 327.825 Million cell updates/sec

US-09-816-989A-4

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

<b>10</b>	Description	membrane spanning	membrane spanning	tolA protein - Esc	histone H1, gonada	tolA protein (impo	sperm tail-specifi	Tola protein PA097	histone H1 - Chlam		Tola colicin impor	histone H1 - sea u	mst101-1 protein -	histone Hi (clone	histone H1-gamma,	hypothetical prote	hypothetical prote	histone H1 - sea u	H1.10	histone H1A - Afri	outer membrane pro	probable erythrocy	probable hupB - My	histone H1-beta, e	hypothetical prote	histone H1 homolog	zuotin - yeast (Sa	hypothetical prote	whe	R27-2 protein - Tr
SUMMARIES	ID	F90725	G85576	JV0057	HSURIP	AG0592	S51364	E83525	859589	G64064	AC0138	806388	S34153	T06241	A26721	AE1689	AE1317	A25550	A28456	HSXL1A	B43592	T09127	G70673	A28100	T17698	S61926	S25194	T06636	822322	T30296
	<u>B</u> B	7	~	~	Н	~	~	N	~	~	~	~	~	~	~	7	~	7	~	Н	~	~	~	~	7	~	N	N	N	0
	Query Match Length	394	394	421	248	376	1390	347	231	372	388	206	344	284	217	243	239	210	220	209	384	1701	214	211	311	182	433	924	236	1128
٠	Query Match	42.3	42.3	41.9	39.3	39.1	38.8	38.2	37.7	37.5	37.4	36.9	36.7	36.1	35.9	35.8	35.6	35.5	35.1	34.8	34.2	34.2	33.9	33.5	33.2	32.9	32.7	32.6	32.4	32.4
	Score	132.5	132.5	131	123	122.5	121.5	119.5	118	117.5	117	115.5	115	113	112.5	112	111.5	111	110	109	107	107	106	105	104	103	102.5	102	101.5	101.5
	Result No.		7	e	4	ហ	9	7	60	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56		28	29

histone H1 - rainb	translation initia	histone H1A - Afri	histone H1.11L - c	conserved hypothet	histone H1 - musco	histone H1-II - Vo	cytosolic repetiti	histone H1 (clone	tolA protein VC183	arylesterase-relat	histone H1.03 - ch	histone H1 - trout	histone H1B - Afri	histone H1B - Afri	histone H1.C - Afr
HSTRIR	E64114	151227	B28456	E75383	801262	JN0748	A44993	T06257	A82152	G87675	D28456	HSTR1	HSXL1B	151447	833219
7	~	N	7	N	~	N	~	N	N	N	~	-	Н	~	~
206	829	229	225	581	218	241	328	288	356	438	224	194	219	220	221
32.3	32.3	31.8	31.6	31.6	31.5	31.5	31.5	31.3	31.2	31.2	31.0	30.8	30.8	30.8	30.8
101	101	99.5	66	66	98.5	98.5	98.5	86	97.5	97.5	97	96.5	96.5	96.5	96.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

-	RESULT 1	
-	F90725	
_	membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain F	ostrain F
	C;Species: Escherichia coli	
_	C;Date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text change 18-Jul-2001	
-	C;Accession: F90725	
	R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.	m, C.G.
_	gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
_	DNA Res. 8, 11-22, 2001	
	A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom	and genon
	A;Reference number: A99629; MUID:21156231; PMID:11258796	
	A; Accession: F90725	

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-394 «HMX>
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774

9. Length 394; Query Match
42.3%; Score 132.5; DB 2; Length
Best Local Similarity 58.9%; Pred. No. 0.00099;
Matches 43; Conservative 8; Mismatches .13; Indels

4.

g

|||| |:|| :| 214 EKAAADKKAAEKA 226 99 55 AKAAA-KEAAYEA ò 셤

RESULT 2 G85576 membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain 1 C;Species: Escherichia coli

Cipate: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Nov-2001
C;Accession: G8550 
K;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85576
A;Audlecule type: DNA

A;Residues: 1-394 <STO> A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09 A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:

A;Gene: tolA

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A;Accession: A91090
A;Aolecule type: protein
A;Rolecule type: protein
A;Rolecule (A)
A;Rolecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tolla protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) (Species: Salmonella enterica serovar Typhi (strain CT18) (Species: Salmonella enterica serovar Typhi (strain CT18) (Species: this species has also been called Salmonella typhi (Spate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 (Spate: 09-Nov-2001 #text_change 09-Nov-2001 (Spate: 09-Nov-2001 #text_change 09-Nov-2001 (Spate: 13. 800-852) (Spate: 13. 800-852, 2001 (Spat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S51364
sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Biochem. 225, 1089-1095, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AKKKAEAEAAKAAAEAKKKAEAEAKAKAADAKKKADAEAAKAAAEAKKKADAAAAK--- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KYAKKEKAYAKAKAEAKAAKKA-KAEAKKYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKA---KKAEAKAAK------KAKAEAKKYAKAEKKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
A;Reference number: A91090; MUID:80156831; PMID:67609
A;Contents: sequence of residues 1-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 122.5; DB 2;
Pred. No. 0.0058;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%; Score 123; DB 1; 56.1%; Pred. No. 0.0039; iive 7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: A91091
A,Molecule type: protein
A,Residues: 80-248 <ST2>
A,NOLE: 144-Arg was also found
C,Superfamily: histone H1
C,Keywords: DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.1%;
51.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.3
Best Local Similarity 56.1
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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C(Species Escherichia coll.)
R(Species I C(Species I R.E.)
R(Species I C(Species I R.E.)
R(Species I R.E.)
R(
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C;Species: Parechinus angulosus (angulate urchin)
C;Species: Parechinus angulosus (angulate urchin)
C;Species: Janar-1980 #sequence revision 31-Mar-1980 #text_change 16-Feb-1997
C;Accession: A91090; A91091; A02586
R;StricMand, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B. Bur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang
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                                                                                                                                                                                               1 AKKYAKKEKAYAKAAKKAEAKKAKAEAKKYAKAA-----KAEKKEYAAAEAKYKAEA 54
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          Length 394;
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Score 132.5; DB 2;
Pred. No. 0.00099;
8; Mismatches 13;
     42.3%;
58.9%;
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                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                                                                                                                                          55 AKAAA-KEAAYEA 66
                                                  Local Similarity
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Query Match
Best Local S:
Matches 43,
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1 AKKYAKKEKAYAKAKKAEAKKAKAKAKAKAKAKA-----AKAEKKEYAAAEAKYKAE 53
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Best Local Similarity 55.6%;
Matches 35; Conservative
                                                                                                                     A,Molecule type: DNA
A,Residues: 1-231 <FAB>
A,Cross-references: EMBL:U16726
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KSA 221
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Accession: E83525
A;Accession: E83525
A;Status: preliminary
A,Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei. A,Reference number: S51364; MUID:95045538; PMID:7957199
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A;Experimental source: strain PA01
C;Genetics:
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C;Species: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tola protein Pa0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                        A,Reference number: S34153
A,Accession: S34153
A,Accession: S34154
A,Molecule type: DNA
A,Roblecule type: DNA
A,Residues: 1-163,'E', 164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A,Cross-references: EWBL:X73481; NID:g313201; PID:g313202
C,Genetics: A,Gene: mst101(2)
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38.2%; Score 119.5; DB 2;
Best Local Similarity 51.5%; Pred. No. 0.0094;
Matches 34; Conservative 7; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
38.8%; Score 121.5; DB
Best Local Similarity 59.7%; Pred. No. 0.019;
Matches 37; Conservative 3; Mismatches :
                                                                      A,Accession: S51364
A,Status: nucleic acid sequence not shown
A,Rolecule type: DNA
A,Residues: 1-1390 «NEE>
A,Cross-references: EMBL:X73481
A,Roesen, J : Heinlein, U.A.O.; Buenemann, H. Submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: FlyBase: FBgn0011816
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histone H1 - Chlamydomonas reinhardtii
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A; Residues: 1-347 <STO>
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A/Reference number: S59581; MUD:96120862; PMID:8590479
                                                                                                                                                                                                                                                                                  A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A;Pascription: The organization, structure and controlling elements of Chlamydomonas hist
A;Reference number: S62122
A;Accession: S62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: G64064; UC5212
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, R;Gocayne, J.D.; Adams, M.D.; Whirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.W.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-372 <TIGR>
A; Cross-references: GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; R; Sen, K.; Sikkema, D.J.; Murphy, T.F.
R; Sen, K.; Sikkema, D.J.; Murphy, T.F.
A; Tib. 75-81, 1996
A; Tib. 1801ation and characterization of the Haemophilus influenzae tolQ, tolR, tolA A; Reference number: JC5212; MUID:97080550; PMID:8921895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C,Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:G571479; PIDN:AAA98452.1; PID:g571480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 КАБККРКААКРАККТТККАААКРКАЕККРКАААКРКАБККРКААКРКАЕККАКААКРААК 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYAKKEKAYAKAKKAEAKAAKKAKAEAK-KYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Superfamily: histone H1
C,Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 2
Pred. No. 0.009;
5; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain 1479
A;Note: the authors translated the codon CGT
                                                                                                                                                    A,Status: nucleic acid sequence not shown A,Molecule type: DNA
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histone H1 (clone TH315) - wheat
C;Species: Triticum aestivum (common wheat)
C;Species: Triticum aestivum (common wheat)
C;Accession: 10-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
C;Accession: T66241
R;Tacka, K.; Ohtsubo, N.; Fujimoto, Y.; Mikami, K.; Meshi, T.; Iwabuchi, M.
Plant Cell Physiol. 39, 294-306, 1998
A;Title: The modular structure and function of the wheat H1 promoter with S phase-specif,
A;Reference number: Z15562; MUID:98249625; PMID:9588026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Datesion: A26721
R;Knowles, JA; Lai, Z.C.; Childs, G.J.
R;Knowles, JA; Lai, Z.C.; Childs, G.J.
A;Title: Isolation, characterization, and expression of the gene encoding the late histor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-284 <TAO>
A;Cross-references: EMBL:D87064; NID:g2980890; PIDN:BAA25203.1; PID:g2980891
A;Experimental source: clone TH315
                      Species: Drosophila hydei
Species: Drosophila hydei
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AKKEKEAAEKKKC-AEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAYAKAKKAEAKAAKK--AKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.021;
-haa 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.1%; Score 113; DB 2; Length 28 llarity 52.5%; Pred. No. 0.026; Conservative 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                A,Cross-references: EMBL:X73480; NID:g313199; PID:g313200 C,Genetics: A,Gene: FlyBase:Dhyd/mst101 A,Cross-references: FlyBase:PBgn0011816 C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AKKEKAYAKAKAEAKAAKKAK--AEAKKYAKAAKAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: T06241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                           C; Species: Drosophila hyde;
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-19
C; Accession: 834153
R; Neesen, J; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
A; Reference number: 834153
A; Accession: 834153
A; Accession: By Actual A; Accession: 134453
A; Reference number: 134458
                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.7%; Score 115; DB
49.4%; Pred. No. 0.02
tive 4; Mismatches
  mst101-1 protein - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 KCAEAAKKEKEAAEKKKCAEA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 YKAEAAK----AAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 72/3
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 32; Conserva
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histone H1-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 K 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                          RESULT 10
AC0138
Tolla control import membrane protein [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0138
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Accession: AC0138
A;Accession: AC0138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Residues: 1-388 <KUR>
C;Genetics: Dramanary
A;Cross-references: GB:ALS90842; PIDN:CAC89966.1; PID:g15979190; GSPDB:CN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
S09388
histone H1 - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Species: Parechinus angulosus (angulate urchin)
C;Accession: S09388
B;Hill, C.S.; Martin, S.R.; Thomas, J.O.
EMBO J. 8, 2591-2599, 1989
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chrom A;Reference number: S09388; MUID:90060019; PMID:2583125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAYAKAK----KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4%; Score 117; DB 2; Length 388;
49.3%; Pred. No. 0.016;
tive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KYAKKEKAYAKAKKAEAK---AAKKAKAEAKKYAKAAKAEKKEYAA----
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Pred. No. 0.013;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.9%;
nilarity 49.4%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-206 <HIL>
C;Superfamily: histone HI
C;Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||| | || :|
172 KKKTAAKKAKKPAAKKA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 49.38
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 YKAEAAKAAAKEAAYEA
                                                                                                                                     228 AEAKAATEAKRKA 240
                                                                                   54 AAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :||
219 KAAADAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 38
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A; Reference number: A26721; MUID:87172742; PMID:3031476

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RESULT 15
AE1689
hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
C; Species: Listeria innocua
C; Date: 27-Nov-2001
C; Accession: AE1689
C; Accession: AE1689
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshil, H. Science 224, 4849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AE1689
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-243 cGLA>
A; Cross-references: GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:GN00178
A; Excentimental source: strain Clip11262
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEK----AYAKAKKAEAK------AAKKAKAEAKKYAKAAK---AEKKEYAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAE--AKYKAEAAKAA 58
A,Accession: A26721
A;Molecule type: DNA
A;Residues: 1-217 <KNO>
A;Cross-treences: 08:M16033; NID:g161517; PIDN:AAA30059.1; PID:g161518
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
F;2-217/Product: histone H1-gamma, embryonic #status predicted <MAT>
                                                                                                                                                                                                                              Query Match 35.9%; Score 112.5; DB 2; Length 217; Best Local Similarity 49.4%; Pred. No. 0.023; Matches 38; Conservative 3; Mismatches 21; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 KPAKKAAKPAKRAAKPA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 AEAKYKAEAAKAAAKEA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AKEAAYEA 66
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Search completed: March 10, 2003, 12:28:27 Job time : 19.3544 secs

170 KEKAAAEA 177

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GenCore version 5.1.3
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01; Search time 15:038 Seconds (without alignments) 182.035 Million cell updates/sec Run on:

US-09-816-989A-4 313 1 AKKYAKKEKAYAKAKAEAK......BAKYKAEAAKAAAKEAAYEA 66 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

	Description	ı	702636 pareculnus	P50600 pseudomonas		-		_		Q9xb18 mycobacteri		P06892 xenopus lae	_	_					Q93mh5 klebsiella	P50887 drosophila	-	_				_	volvox	-	salmo	P15866 xenopus lae	m	5 schizo	P09987 gallus gall
SUMMARIES	ID	TOLA ECOLI	MST2 DROHY	TOLA PSEAE	TOLA HAEIN	MST1_DROHY	HIG_STRPU	DBH_MYCSM	H1_LYTPI	DBH_MYCBO	H110 CHICK	HIA_XENLA	TMPB_TREPH	H1 WHEAT	DBH MYCTU	RS6_AEDAL	H1B_STRPU	ZUOI YEAST	ASR_KLEPN	RL22 DROME	H1_ONCMY	H1B CHITE	IF2_HAEIN	RS6_AEDAE	H11L CHICK	H1_ANAPL	H12 VOLCA	H103 CHICK	H1_SALTR	HIC1 XENLA	-	ъ,	H1_CHICK
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de	Query Match	41.9	9.00	38.2	7.	36.7	35.9	35.6	35.5	35.3	٠	4.	34.2	4.	ω.	ω.	33.5	32.7	32.6	32.6	32.3	32.3	32.3	32.1	31.6	31.5	31.5	31.0	30.8	ö	ö	30.8	30.7
	Score	131	121.5	119.5	117.5	115	112.5	111.5	111	110.5	110	109	107	106.5	106	106	105	102.5	102	102	101	101	101	100.5	66	98.5	98.5	97	96.5		96.5	96.5	96
	Result No.	н с	N (1)	4	ß	9	7	ω	თ	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

P40277 chironomus P15867 xenopus lae P4075 chironomus P40278 chironomus P12036 homo sapien P60284 gallus gall P40263 glyptotendi P26569 arabidopsis P16401 homo sapien P40266 glyptotendi P4026 glyptotendi P4026 glyptotendi P80288 gallus gall
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# ALIGNMENTS

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Strickland M., de Groot P.C., von Holt C.,
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InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; Linker histone; I.
ProDom; PD000373; Linkerhist N; 1.
                                                                                                                                      cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 56.1 tes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144
  Strickland W.N., Str:
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 KAAKKA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MST2 DROHY
Q08696;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKAK-----KAEAKAAKKAKAEAKKYAK-----AAKAEKK-EYAAAEA 48
                                                                                                                                                                                                                                                                                                                                                                   OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                        MEDLINE-99332679; Pubmed=10404600; Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; Indiamenous phage infection: crystal structure of g3p in complex with its coreceptor, the Cterminal domain of TolA."; Structure 7:711-722(1999).

-- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels 12;
                              "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131; DB 1; Length 421; Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1, gonadal.
Parechinus angulosus (Angulate sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa, Echinoidea, Euechinoidea, Echinoidea, Echinoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (2,4).
8B2F52B4B97C655E CRC64;
                                                                                                          X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-84.
MEDLINE=80156831; PubMed=6767609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M28232; AAA24683.1; -. EMBL; AE000177; AAC73833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
PDB; ITOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.9%;
52.6%;
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34
421
421
278
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Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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P02256;
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SEQUENCE OF 80-248.
MEDINE-80155832; PubMed-7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 KKAKKTSAAAKAKKAKAKARARKARKAKAAAAKRKAALAKKKAAAAKRKAAAKKAKKKK 179
"The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                 "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and the entire primary structure.";

Eur. J. Biochem. 104:567-578 (1980)

-!- FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MST101(2).
Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KYAKKEKAYAKAKKAEAKAAKKA-KAEAKKYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95045538; PubMed=1957199;
Neesen J., Padmanabhan S., Buenemann H.;
Nandemly arranged repeats of a novel highly charged 16-amino-acid motifi representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila hydei.";

Eur. J. Biochem. 225:1089-1085(1994).

-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.

-i- SUBCELLULAR LOCATION: Cytoplasmic.

-i- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 123; DB 1; Length 24 56.1%; Pred. No. 0.0016; Live 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AA; 26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: SPERM.
-i- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; A02586; HSURIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
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FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                 347 AA;
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                       (Potential).
                                                                                                                                                                                                                                                     209
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215 AARKAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                             58 AAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOLA OR HI0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TolA protein.
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                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                          DOMAIN
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBo.sib.ch).
                                                                                                                                                                                                                                                                                                       ë,
           DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELLCAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=LO43137; Pubmed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Weetbrock-Wadman S., Yuan Y., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen."
                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                      656 KKLAKKEKBTAEKKKCE-KAAKKRKEAAEK-KKCAEAAKKEKEAAEKKKCEEAAK-KEKE 712
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                             KKYAKKEKAYAKAKKAEAKAAKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKE 61
                                                                                                                                                                                                                 Sperm; Repeat; Multigene family; Polymorphism.

DOMAIN 332 1268 59 X.16 AA APROXIMATE TANDEM REPEATS

SEQUENCE 1391 AA; 159000 MW; 1B2A368F30F48878 CRC64;
                                                                                                                                                                                                                                                                             Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolORA genes of
                                                                                                                                                                                                                                                                             Score 121.5; DB 1; Length
Pred. No. 0.0086;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                          EMBL; X73481; CAA51876.1; -.
PIR; S34154; S34154.
FlyBase; FBgn0020733; Dhyd\mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                              38.8%;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.7*
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
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SPERMATIDS
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P50600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=RG / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; DubMed=7542800;

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAK---KEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iransport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
(BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 119.5; DB 1; Length 347; 51.5%; Pred. No. 0.0039; tive 7; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL)
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 CY
37 PO
347 PE
216 PO
37935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004530; AAG04360.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 34; Conservative
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PIR; A26721; A26721
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                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neesen J., Buenemann H., Heinlein U.A.,
"The Drosophila hydei gene Dhmst101(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Dev. Biol. 162:414-425(1994).
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7224,
                                                                                                                                                                          Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
         (BY SIMILARITY).
SUBCELLUIAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                            AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKA-----AKAEKKEYAAAEAKYKAE
 FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
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V -> A (IN STRAIN 1479).
A -> A (IN STRAIN 1479).
A -> AKAABEAKAKA (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
L -> P (IN STRAIN 1479).
I -> V (IN STRAIN 1479).
N -> S (IN STRAIN 1479).
                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
                                                                                                                                                                                                                                                                                                                                -> S (IN STRAIN 1479).
-> A (IN STRAIN 1479).
-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                    1479)
                                                                                                                                                                                                                              V -> A (IN STRAIN
K -> R (IN STRAIN
A -> P (IN STRAIN
                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 117.5; DB 46.6%; Pred. No. 0.0059;
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Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 31, Last sequence update) (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                                                                                                                                                                    PERIPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94200512; PubMed=8150205;
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                                                                                                                                                                                                                                                                                                                                                       333 8
39831 MW;
                                                                                                                                   EMBL; U32470; AAC22041.1; -. EMBL; U32470; AAC44596.1; -.
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Drosophila hydei (Fruit fly).
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190
223
232
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254
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323
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254
306
323
333
372 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                       Complete proteome
                              (Potential).
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16-OCT-2001
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87172742; PubMed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; Medels J.A., Lai Z.-C., Childs G.J.; "Isolation, characterization, and expression of the gene encoding the late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                            DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL. POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS
FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purpuratus.";
Mol. Cell. Biol. 7:478-485(1987).
--- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
--- SUBCELLULAR LOCATION Nuclear.
--- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                             yy similarity).
IN SPERMATOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 344;
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Pred. No. 0.0087;
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01-AUG-1988 (Rel. 08, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Scor.
49.4%; Pred. No. v...
4; Mismatches
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                                                                (By
                              ASSOCIATED WITH AXONEMAL STRUCTURES. SUBCELLULAR LOCATION: Cytoplasmic (B) TISSUB SPECIFICITY: TESTIS. LOCATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X73480; CAA51875.1; -.
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                                                                                                                                 SPERMATID BUNDLES
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NCBI_TaxID=7668;
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us-09-816-989a-4.open.rsp

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                          35.5%; Score 111; DB 1; Length 210;
48.6%; Pred. No. 0.012;
tive 4; Mismatches 23; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 АКККЕОКЕККААКТКАRКЕКLAAKKAAKKAAKKYKRPAKAKKPAKKAAKKPAAKKAA-К 171
                                                                                                                                                                                                                                                                                                                                                           Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
-----AKKAEAKA-AKKA--KAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X04488; CAA28177.1; -.
PIR; A25550; A25550.
HSSP: P02259; 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; Linker histone; I.
ProDom; PD000373; Linkerhist N; 1.
SmART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAK-----AKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                      210 AA.
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                                                                                                                           -AATKAPAKKAAAKAPAKKAATKA 191
                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
                                                                                  43 YAAAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 48.6
Matches 35; Conservative
                                                                                                                                                                                                                                      STANDARD;
  1 AKKYAKK---EKAYAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 KPAAKKPAKKAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 AEAAKAAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                              Late histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lytechinus
                                                                                                                                                                                                                                    H1 LYTPI
P06144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                             169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
DBH MYCBO
ID DBH M
AC Q9XE1
DT 16-OC
DT 16-OC
                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                139 AKKATKKTKKVKKPAAKKAKKPAAKKPAAKKPAKKAKKPAKKVAKPAKKAAAKPAKAAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                               1 AKKYAKKEK----AYAKAKAEAK-----AAKKAKAEAKKYAKAAK---AEKKEYAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
           InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst N.
Pfam; PF00538; linker histone; I.
Probom; PD000373; Linkerhist N; I.
SWART; SM00526; H15; I.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAO1. Gen. Genet. 260:475-479(1998).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-AFTCC 700084 / mc(2)155; STRAIN-AFTCC 700084 / mc(2)155; MEDLINE=99110209; PubMed=9894918; Lee B.H., Murugasu-Oel B., Dick T.; "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                       // Match 35.9%; Score 112.5; DB 1; Length 217; Local Similarity 49.4%; Pred. No. 0.0093; neg 38; Conservative 3; Mismatches 21; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
HUP OR HLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGENERAL HISTONE-LIKE DOMAIN.
DEGENERATE REPEATS REGION.
CASPS77F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.6%; Score 111.5; DB 1; Length 2
50.0%; Pred. No. 0.011;
ive 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; DNA condensation; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Arversor.
HSSP; P02346; 1HUU.
InterPor; IPR000119; Bac DNAbind.
Pfam; PF00216; Bac DNA binding; 1.
ProDom; PD000945; Bac DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00045; HISTONE_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF068138; AAD13809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AA; 21230 MW;
                                                                                                                                                                                                                                                                                                                                                                                          || |: || || |
199 KPAKKAAKPA 215
                                                                                                                                                                                                                                                                                                                                                                  46 AEAKYKAEAAKAAAKEA 62
                                                                                                                                                                                                                                    Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 42; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        smegmatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBH MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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DBH_MYCSM
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7

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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (GENE CLUSTER X1H3).
MEDLINE=86037224; PubMed=3863963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001386; Histone H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00538; linker histone; 1. ProDom; PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M17018; AAA48788.1; -.
                                                                                                                                                        IDENTIFICATION OF ALA-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 1
219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A28456; A28456.
HSSP; P08287; IGHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                        SEQUENCE FROM N.A.
                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetylation.
INIT MET
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mc.
Local 5.
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H1A XENLA
P06892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                     from Mycobacterium.",
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENY ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                         Prabhakar S., Tyagi J.S., Prasad H.K.;
"HLPMt-A target for differentiation of M.tuberculosis and M.bovis.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK---EKAYAKAKKAEAKA-AKKA--KAEAKKYAKAAKAEKKEYAAA----- 46
                                                      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                          Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T., "Identification of a novel protein generating bacterial slow growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1).
Gallus gallus (Chicken).
ENkaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%; Score 110.5; DB 1; Length 205; 47.0%; Pred. No. 0.013;
          DNA-binding protein HU homolog (Histone-like protein) (Hlp) HUP OR HLP OR MDP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 DEGENERATE REPEATS REGION.
199 A -> T (IN REF. 2).
21262 MW; 19FCE67885DFE6A8 CRC64;
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y18421; CAB46493.1; -.
EMBL; AB013441; BAA78330.1; -.
HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001386; HisTone H1/H5.
Pfam; PF00216; Bac DNA binding; 1.
PRINTS; PR00624; HISTONEH5.
ProDom; PD000945; Bac DNAbind; 1.
SWART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 SVRKAATKAPAKKAAAKRPATKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EAKYKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 1
205 AA;
                                                                                                                                                                                                             STRAIN=BCG / Tokyo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 39; Conserv
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=1765;
                                                                                                                            STRAIN=ANS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H110_CHICK

D H110_CHI

AC P08256;

DT 01-NUG-1

DT 15-UL-1

DE Histone

OS Gallus 9

OC ENkaryot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKE 61
MEDLINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia; Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                         MEDLINE=98060905; PubMed=9396815; Schwarz S., Hess D., Jost J.P.; IMDR-2-H1) consists of histone H1 subtypes which are truncated at the C-terminus."; Nucleic Acids Res. 25:5052-5056(1997).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR: BELONGS TO THE HISTONE H1/H5 FAMILY.
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109 GLOBULAR.
21872 MW; A944DF6COD3048AE CRC64;
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42677 MW;
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  LARGE MOLECULES
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384 AA;
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237 AARKAAEEAA 246
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  AXX OCC OCC DE TANK
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MEDLINE-91372983; PubMed=1894368;
MEDLINE-91372983; PubMed=1894368;
Sithon D.B., Limberger
Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.;
"Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpB and TmpB proteins";
Infect. Immun. 59:3685-3693(1991).
-i- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
                "Genomic organization and nucleotide sequence of two distinct histone gene clusters from Xenopus laevis. Identification of novel conserved upstream sequence elements.";
                                                                                                                SEQUENCE FROM N.A.

Perry M., Thomsen G.H., Roeder R.G.;
"Genomic organization and nucleotide sequence of two distinct histone gene clusters from Xenopus laevis: Identification of novel conserved
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Pfam; PF00538; linker histone; 1.
Probom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
                                                                                                                                                                                            upstream sequence elements.";
J. Biol. Chem. 260:479-499(1985).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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NCBI TaxID=162;
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Perry M., Thomsen G.H., Roeder R.G.;
                                                                             . Mol. Biol. 185:479-499(1985).
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173 PAKKTA 178
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238 AA; 24222 MW; 2CBIC16899B65A27 CRC64;
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15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein H homolog (Histone-like protein) (Hlp) (21-kDa laminin-2-binding protein).
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                 STRAIN=CV. Horoshirikomugi; TISSUB=Seedling;
MEDLINE=92020152; PubMed=1923777;
Yang P., Kateura M., Nakayama T., Mikami K., Iwabuchi M.;
"Molecular cloning and nucleotide sequences of cDNAs for histone land HIB variants from wheat.";
Nucleic Acids Res. 19:5077-5077(1991).
                                                                                                                                                                                                                                   Morisawa G., Meehi T., Iwabuchi M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES HI ARB NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
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InterPro; IPR003216; LinkerhIst_N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist.
SMART; SM00526; H15; I.
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                                                                                                                                                                                                          STRAIN-CV. Horoshirikomugi,
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197 AKKA 200
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P95109;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                          STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
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DNA-binding; DNA condensation; Repeat; Complete proteome.
DOMAIN 1090 BACTERIAL HISTONE-LIKE DOMAIN.
DOMAIN 101 214 DEGENERATE REPEATS REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA; 22187 MW; CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 ÁVKKTAVKASVRKÁATKÁPÁKKÁAÁKRPÁTKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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EMBL; AE007127; AAK47393.1; -
HSSP; P02346; 1HUU.
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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model
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March 10, 2003, 12:15:01 ; Search time 34.9494 Seconds
 (without alignments)
 389.109 Million cell updates/sec Run on:

US-09-816-989A-4

Perfect score:

313 1 AKKYAKKEKAYAKAKKAEAK.......EAKYKAEAAKAAAKEAAYEA 66 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 0B DB Minimum I Maximum I

SPTREMBL Database

sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\* sp\_archea:\* sp\_bacteria:\* sp\_fungi:\* sp\_human:\*

sp\_unclassified:\*
sp\_rvirus:\* sp\_virus:\*
sp\_vertebrate:\* sp\_bacteriap:\* sp archeap:\*

sp\_plant:\* sp\_rodent:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	·	Description	Q8x965 escherichia	Q9cm70 pasteurella	Q8zqt6 salmonella	Q9wwx1 pseudomonas	Q8z8c1_salmonella	Q937k4 erwinia chr	Q8zgz2 yersinia pe	001395 drosophila	O65794 triticum ae	Q92a67 listeria in	Q8y5w4 listeria mo	Q39576 chlamydomon	Q9xh19 triticum ae	Q98kg7 rhizobium l	Q9h8h4 homo sapien	Q9h9fl homo sapien
		E .	Q8X965	Q9CM70	O8ZQT6	Q9WWX1	Q8Z8C1	Q937K4	Q8ZGZ2	001395	065794	Q92A67	Q8Y5W4	039576	O9XHL9	Q98KG7	Q9H8H4	<b>Q9Н9</b> F1
		8	16	16	16	0	16	7	16	Ŋ		16	16	10	10	16	4	4
		Match Length DB	394	389	407	372	376	395	388	275	284	243	239	232	275	1341	198	467
d	Query	Match	42.3	40.4	39.8	39.1	39.1	38.3	37.4	36.3	36.1	35.8	35.6	35.3	35.1	35.1	34.7	34.7
		Score	132.5	126.5	124.5	122.5	122.5	120	117	113.5	113	112	111.5	110.5	110	110	108.5	108.5
	Result	No.	1	7	Э	4	'n	9	7	80	6	10	11	12	13	14	15	16

	Q8xvn7 ralstonia s	O61164 plasmodium	Q98wu3 triticum ae	Q9swu2 triticum ae	Q8y1f6 ralstonia s	Q9fp71 oryza sativ	Q9uv33 ascobolus i	Q52088 pseudomonas	Q84528 paramecium	Q8t5c8 plasmodium	Q45370 bordetella	. Q99kc2 mus musculu	Q90zd7 bufo bufo g	Q9uan1 drosophila	Q8rxd0 arabidopsis	Q9su08 arabidopsis		Q9ndi9 plasmodium			093946 candida alb	Q91369 xenopus lae	Q9ru45 deinococcus		Q23784 chironomus	_	Q25636 parechinus
Q9SWU1 Q9XHL8	Q8XVN7	061164	Q9SWU3	Q9SWU2	Q8Y1F6	Q9FP71	Q9UV33	Q52088	084528	QBT5CB	Q45370	Q99KC2	Q90ZD7	Q9UAN1	QBRXD0	800S60	Q9KJ98	6IQN6Ö	026947	099281	093946	091369	Q9RU45	018319	023784	Q9V6S7	<b>Q25636</b>
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227	200	1701	236	237	345	755	213	298	311	1866	182	436	224	312	485	924	629	696	1128	166	212	229	581	233	243	607	180
34.3	34.2	34.2	34.0	34.0	34.0	34.0	33.5	33.2	33.2	33.2	32.9	32.7	32.6	32.6	32.6	32.6	32.4	32.4	32.4	32.1	31.8	31.8	31.6	31.5	31.5	31.5	31.3
107.5	107	107	106.5	106.5	106.5	106.5	105	104	104	104	103	102.5	102	102	102	102	101.5	101.5	101.5	100.5	99.5	99.5	66	98.5	98.5	98.5	98
17	19	20	21	22	23	24	52	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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[2]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=2156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Handa T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Bscherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res 8:11-22(201).
EMBL; AR002552; BAB34197.1; -.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TOLA OR ECS0774.
Bacterichia coli 0157:H7.
Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                       394 AA.
                                     PRT;
                                       PRELIMINARY;
                                                                                                                                                                                                                                                           NCBI_TaxID=83334;
                                     Q8X965
Q8X965;
RESULT 1
                      08x965
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL, AE006135, AAK03052.1; -...
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JNN-2002 (TrEMBLrel. 21, Last annotation update)
Tol protein, membrane spanning protein.
Tol.A OR SYMO747.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                           9;
                                                                                                   DB 16; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126.5; DB 16; Length 389;
Pred. No. 0.0017;
9; Mismatches 12; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                 Query Match 42.3%; Score 132.5; DB 16; Length Best Local Similarity 58.9%; Pred. No. 0.00053; Matches 43; Conservative 8; Mismatches 13; Indels
                                                           5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                389 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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MEDLINE=21145866; PubMed=11248100;
Tir. Paust
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000533; Tropomyosin. PROUTS; PRO1919; TROPOMYOSIN. Complete proteome. SEQUENCE 389 AA; 42197 MW; B40
                                                           394 AA; 40517 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AEKAKADAEAAQRKA 257
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214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                    55 AKAAA-KEAAYEA 66
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                                        Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=747;
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NCBI_TaxID=602;
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                                                         SEQUENCE
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QBZQT6
QBZQT6
QBZQQ AC
QBZQQ OI-M
DT 01-M
DT 01-M
DT 01-M
DT 701-M
CO Salm
CO
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 АКККАБАБААКАААБАКККАБАБААКААВАВКККАПАБААКАААБАКККАПЛААААК---- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
J. Bacteriol. 178:1699-1706(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKA---KKAEAKAAK-----KAKAEAKKYAKAAKAEKKEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL mull mutant of Pseudomonas putida.";
"Characterization of an OprL mull mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
EMB. X74218; CAB50780.1;
InterPro; IPR01386; Histone H1/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.8%; Score 124.5; DB 16; Length 407; llarity 47.8%; Pred. No. 0.0026; Conservative 6; Mismatches 10; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 AA; 41865 MW; 2534352116602D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AAAEAKYKAEAA-----KAAAKEAA
                                                                                                                                                                                                                                                                                                                                                EMBL; AE008730; AAL19691.1; -.
InterPro; IPR000104; Antifreeze 1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96422022; PubMed=8824639;
                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
ses 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tola protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MT-2;
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NCBI_TaxID=556;
                                                                                                               STRAIN=3937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        001395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     001395
ID 00
AC 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hen T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.; amultiple drug resistant Salmonella enterica serovar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AKKKAEABAAKAAAEAKKKAEAEAAKAAADAKKKADAEAAKAAAEAKKKADAAAAK---- 228
                                                                                                                                                                                 Gaps
                                                                                                                                           1 AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA--EAAKAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKA---KKAEAKAAK------KAKAEAKKYAKAAKAEKKEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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             DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.1%; Score 122.5; DB 16; Length 51.3%; Pred. No. 0.0036; ive 4; Mismatches 13; Indels
      39.1%; Score 122.5; DB 2; Length ilarity 51.5%; Pred. No. 0.0035; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21534947; PubMed=11677608;
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EMBL; AL627268; CAD05209 1; -.
InterPro; IPR00104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AAADAKKKAAAEKAAAE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 AAAEAKYKAEAAKAAAKE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TolA protein.
TOLA.
Erwinia chrysanthemi.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           205 AEDAKKKA 212
                                                                                                                                                                                                                                                                            59 AKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tola protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CT18;
                                                                            35;
Query Match
Best Local S
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                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
0828C1
1D 0828C1
DD 01-M
DT 0
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0937K4
11D 0937T
AC 09377
DT 01-D)
DT 01-D)
DE TOLA
GN TOLA
GN TOLA
CO BECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L., Barents, Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Persinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.3%; Score 120; DB 2; Length 395;
Best Local Similarity 54.1%; Pred. No. 0.0061;
Matches 40; Conservative 9; Mismatches 13; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKE-----KAYAKAKK-----AEAKAAKKAKAEAKKYAKAAKAE-KKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKYAKKEKAYAKA----KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                   RAY W.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
"characterization of the Erwinia chrysanthemi tol-pal genes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAC82708.1;
SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.4%; Score 117; DB 16; Length 388; Best Local Similarity 49.3%; Pred. No. 0.011; Matches 33; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 AA; 40424 MW; 81447B04B30A7E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tola colicin import membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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01-JUL-1997 (TrEMBLrel. 04, Created)
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InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREZEI.
COMPLEE proteome.
SEQUENCE 388 AA; 40424 MW; 8144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / BIOVAR ORIENTALIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 KKAEAA-AAAKKAA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 YKAEAAKAAAKEAA 63
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 KAAADAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AAAKEAA 63
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4,

1;

2; Gaps

21; Indels

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2 KKYAKKEKAYAKAKKAEAKAAKK - - AKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAA 59
  6; Mismatches
                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein lin2055.
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  Matches 32; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin2055.
Listeria innocua.
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01-DEC-2001 (
01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                                  -! STRILLARITY).
-! SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- TISSUB SPECIFICITY: TESTIS (BY SIMILARITY).
-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
EMBL; UBS627; AABS1369.1; -
FlyBase; FBGM0020732; Dhyd\met101(3).
Sperm; Repeat; Multigene family.
DOMAIN 64 255 13 X 16 AA APPROXIMATE TANDEM REPEATS OF
                               Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Rphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 AKKEKEAAEKKKC-AEAAKKEKERAAEKKKCAEAAKKEQEAAQKKKCAELAKKEKEAAEKK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AKKEKAYAKAKKAEAKAAKKAK--AEAKKYAKAAKAE-------KKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99249625; PubMed-9588026;
Taoka K., Ohtsubo N., Fujimoto Y., Mikami K., Meshi T., Iwabuchi M.;
The modular structure and function of the wheat H1 promoter with S
phase-specific activity.";
Plant Cell Physiol. 39:294-306(1998).
EMBL; D87064; BAA25203.1;
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 36.3%; Score 113.5; DB 5; Length 275; Local Similarity 52.7%; Pred. No. 0.015; Los 39; Conservative 3; Mismatches 15; Indels 17;
                                                                                                                                                                                                                                                                                                     (BY
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                                                                                                                                                                                                                                                 Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76BAA7B2A2DF732C CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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Pred. No. 0.017;
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InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist_N.
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Pfam; PF02178; AT hook; 1.
ProDom; PD000373; Linkerhist N; 1.
SWART; SM00384; AT hook; 1.
SWART; SM00526; H15; 1.
SEQUENCE 284 AA; 29159 MW; 516.
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52.5%;
                   01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        SIMILARITY)
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Radiaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Radiaser P., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Brian K.-D., Fshil H., Garciadel Portillo F., Garrido P.,

Cautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Silmoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

Comparative genomics of Listeria species.";

In Science 294:849-852(2001).

Embl., AL596170; CAC97285.1; -.

REMBL, AL596170; CAC97285.1; -.

Refair PF01476; Lysm.

Pram, PF01476; Lysm.

Refair PF01476; Lysm.

Rypothetical protein; Complete protecome.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                            Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 35.8%; Score 112; DB 16; Length 243; Local Similarity 47.1%; Pred. No. 0.018; Onservative 11; Mismatches 23; Indels
                                                                                              (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 20, Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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ID Q6
AC Q6
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DT 01
DD DT 01
OC B6
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STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Kawashima K., Kimura T.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinhoff S.; "Structural and functional characterization of histone H1 from animal
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.1%; Score 110; DB 10; Length 275; ilarity 48.7%; Pred. No. 0.03; Conservative 5; Mismatches 20; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and plant cells.";
Thesis (1998), University of Goettingen, Humboldtallee.
EMBL; AF07024; AAD41007.1; -.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhīst_N.
Pfam; PF00538; linker histone; 1.
PRINTS; PR00624; HISTONEHS.
Propom; PD000373; Linkerhist_N; 1.
SMART; SM0626; H15; 1.
SEQUENCE 275 AA; 27793 MW; B96DB4B710FF188F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll1482.
                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                            275 AA
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                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                         PRT;
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205 PKAEKKAKAAKPAAKKSA 222
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Triticum aestivum (Wheat).
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                                                              46 AEAKYKAEAAKAAAKEAA
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Best Local Similarity
Matches 37; Conserv
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                                                                      MEDILINE-21537279; PubMed=1162669;
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Gautier L., Geobel W., Garcia-Chopez N., Hain T., Hauf J., Duskoron D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., Schmitt R.;
Chlamydomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHI.
Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=96120862; PubMed=8590479; Park P.B., Cornelius T., Schmi Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmi The organization structure and regulatory elements of Chlamydom histone genes reveal features linking plant and animal genes."; Curr. Genet. 28:333-345(1995).

EMBL; U16726; AAA98452.1; -.

INTERPRO; PRO259; IHST.

INTERPRO; IPRO01386; Histone H1/H5.

INTERPRO; IPRO03316; Linkerhist N.

Probom; PD000331; Linkerhist N.

Probom; Linkerhist N, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.3%; Score 110.5; DB 10; Length 50.0%; Pred. No. 0.023; Live 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.6%; Score 111.5; DB 16; Length 46.4%; Pred. No. 0.02; ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                  EMBL, ALS91991, CAD0019.1; -.
ListiList; LM001941; -.
InterPro; IRR002482; LysM.
FPfam; PF01476; LysM; 1.
SWART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00526; H15; 1.
SEQUENCE 232 AA; 24693 MW; 2D006AE44ABFA037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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(TrEMBLrel. 01, I
(TrEMBLrel. 20, I
                                                            STRAIN=EGD-E / SEROVAR 1/2A;
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Best Local Similarity 46.4%
Matches 32; Conservative
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Best Local Similarity 50.0°
Matches 39, Conservative
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163 AAEKAAAE 171
                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 AAAKEAAYE 65
  NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002
Histone H1.
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MON-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ13629 fis, clone PLACE1011056, weakly similar to histone H1, gonadal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKAKKAEAKAAK---KAKA---BAKKYAKAA--KAEKKEYAA-AEAKYK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                   8;
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                                                                                                                                                                                        Score 110; DB 16; Length 1341;
Pred. No. 0.14;
9; Mismatches 16; Indels 8
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Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002997; BAB48841...; -.
Hypothetical protein; Complete proteome.
SEQUENCE 1341 AA; 138670 MW; 79C5D8149C969BC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 53.5%;
Matches 38; Conservative
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nes 36; Conservative
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1255 ADAKAAAEQQA 1265
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Search completed: March 10, 2003, 12:25:56 Job time : 35.9494 secs

52 AEAAKAAAKEA 62 |:|:||||| 77 AKAVRAKAKNA 87

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March 10, 2003, 12:15:01; Search time 34.3924 Seconds (without alignments) 255.712 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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313
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Copolymer molecula	Recombinant copoly	Peptide #10 used i	Amino acid polymer	Poly-Lys-Ala used	Nucleic acid trans				
SUMMARIES	ID	AAY82574	AAY82575	AAY82576	AAY82577	AAY82573	AAR06445	AAY98499	AAY59044	AAU04289	AAB45852
	DB	21	21	21	21	21	11	21	21	22	22
	Query Match Length DB	99	77	86	109	26	154	100	100	100	100
de	Ouery Match	100.0	90.3	85.6	73.0	63.3	41.4	40.9	40.9	40.9	40.9
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## ALIGNMENTS

glatiramer acetate, autoimmune disease, antiarthritic, neuroprotective, osteopathic; immunosuppressive; antibyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown s disease, chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. Copolymer; molecular weight marker; TV-marker; immune disease; pemphigus vulgaris; systemic lupus erythematosus AAY82574 standard; peptide; 66 AA. 28-JUL-2000 (first entry) AAY82574; 

Unidentified

06-APR-2000.

WO200018794-A1

99WO-US22402 24-SEP-1999;

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

06-APR-2000.

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                                                                                                                                                                                                                AAV82571 to AAV82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP) which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic manemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uvecretinitis, Crohn's disease, chronic minus thrombocycopaenia purpura, colitis, crontact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxeedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown sidsease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 313; DB 21; Length 66; 100.0%; Pred. No. 3e-24; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                           Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nolecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Conservative
                                                              WPI; 2000-317499/27.
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                    Lis D;
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WO200018794-A1

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight can an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune complete and include either cell-mediated or antibody-mediated diseases and inflammacory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia cureoretinitis, contact sensitivity disease, diabetes mellitus, Graves Compositis, contact sensitivity disease, diabetes mellitus, Graves Compositis, peophoritis, peophoritis, peophoritis, contact sensitivity disease, diabetes mellitus, contact include host-versus-graft disease, graft-versus-profices of the invention have delined molecular weights and physical properties which are analogous to distant marker manner acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
                                                                                                                                                                                                                                                                                                   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 282.5; DB 21; Length 77; 84.4%; Pred. No. 3.6e-21; indels 11; of Mismatches 1; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82576 standard; peptide; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English.
                                                                                                                                                  CO LTD
                                                                                                       98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular weight markers.
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                                                                                                                                                  (YEDA ) YEDA RES & DEV
(TEVA-) TEVA PHARM USA
                                                                                                                                                                                                                                                          WPI; 2000-317499/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 AA;
                                                                                                                                                (YEDA ) YEDA RES
                                                                                                                                                                                                                    Lis D;
                                                               24-SEP-1999;
                                                                                                       25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                  Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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a
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Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

28-JUL-2000 (first entry)

weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antichody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and phylaical properties which are analogous to molecular weights and phylaical properties which are analogous to molecular weights and phylaical properties which are analogous to molecular weights. Crohn's disease, chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedems; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. AAY82571 to AAY82577 represent specifically claimed copolymer molecular Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases inflammatory condition; multiple sclerosis; rheumatoid arthritis; Claim 10; Page 14; 72pp; English. (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. 99WO-US22402. 98US-0101693. molecular weight markers. WPI; 2000-317499/27. WO200018794-A1. Lis D; 25-SEP-1998; Unidentified 24-SEP-1999; 06-APR-2000. Sequence Gad A, 

86 AA;

3; 85.6%; Score 268; DB 21; Length 86; 75.6%; Pred. No. 1.1e-19; ive 0; Mismatches 1; Indels 20; Gaps 1 AKKYAKKEKAYAK----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAKAEKKEYAAAEAK 60 99 -----YKAEAAKAAAKEAAYEA 1 Similarity 75.6 65; Conservative Query Match Local Matches 셤 셤 8 ò

AAY82577 standard; peptide; 109 AA AAY82577; AAY82577 ID AAYE XX AC AAYE XX

RESULT 4

61 YKAEAAKKAYKAEAAKAAKEAAYEA

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; sosteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. 99WO-US22402. 98US-0101693. WPI; 2000-317499/27. WO200018794-A1 Lis D; Unidentified 24-SEP-1999; 25-SEP-1998; 06-APR-2000. Gad A, 

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple soleonis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic uveoretinits, Crohn's disease, functionmune thyroiditis, autoimmune uveoretinits, context sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psendiasis, pemphigus vulgaris, or systemic lupus erythematosus Mediated mediated diseases which can be treated in the context of t defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases have include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention Claim 10; Page 14; 72pp; English

Sequence

molecular weight markers.

4 43; Gaps 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 DB 21; Length 109; Indels Score 228.5; DB 21; Pred. No. 1.2e-15; 0; Mismatches 4; 1 AKKYAKK-EKAYAKAKKA-----EAKAAKKA-----73.0%; Best Local Similarity 56.9%; Matches 62; Conservative Query Match ð 셤

26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA

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5,

10; Gaps

Indels

1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60 1 AKKYAKKEKAY --AEAKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50

80.3%; Pred. No. 5.9e-13; ive 2; Mismatches 1;

53; Conservative

EAAYEA 66

g

63.3%; Score 198; DB 21; Length 56;

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Best Local Similarity
                          Matches
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                                                                                                                                                                                                                                                                                                                                Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive, antithyroid; antiinflammacory; antianaemic; immunosuppressive; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown a disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uveoretinitis, Crohn's disease, chronic immune thrombocycopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barrer's syndrome, Hashimoto's disease, idiopathic myxeedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                     Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft-versus-host disease,
61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .nclude host-versus-graft disease,
                                                                                                                             AAY82573 standard, peptide; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US22402.
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                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999;
                                                                                                                                                                                                                                28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000
                                                                                                                                                                                AAY82573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gad A,
                                                                          RESULT 5
                                                                                                  AAY XX DAY XX DA
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coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidaes, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleaved of the fusion protein. The product prevents or arrests experimental autoimmune encephalonyelliss. They are used to prevent, arrest or control a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geneg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encephalomyelitis. They are used to prevent, arrest or control edemyellnating disorder, e.g. multiple soleroais. They may also be used as additives to air care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.4%; Score 129.5; DB 11; Length 154; 48.8%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        To improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
                                                                                                                                                                                                                                                                                                                                                                                     Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                   AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 11, 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90EP-0301700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0473845.89US-0312541.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-255848/34.
N-PSDB; AAQ05664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunological activ.
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ05665
EAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1990;
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17-FEB-1989;
                                                                                                                                                                                                                                                                                                                    03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1990,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                    AAR06445;
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                    21
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                ë.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                Gaps
                                                KKYAKKEKAYAKAKKAEAKAAKKAKAEA-----KKYAKAAKAEKKEYAAAEAKYKA 52
                                                                   Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 128; DB 21; Length 100;
Pred. No. 9.3e-06;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÿ
              7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith
                                                                                                                                                                                                                                                                                                                                               Peptide #10 used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Column 125-128; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cristiano RJ,
                                                                                                                                                                                                                                       AAY98499 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE,
                                                                                                                                      || :| || || EAEEAEYKKYKKKAKKKKK 117
                                                                                                                   EAAKA-----AAKEAAYE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.7%;
Matches 42; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                              (first entry)
              39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-281993/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gottchalk S,
                                                                                                                                                                                                                                                                                                            31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6033884-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                          AAY98499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Matches
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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to Scomponents: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytopissm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting especific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells animal model. The NTS can be used in vitro with tissue culture cells specific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Lys-Ala in positions 3 to 100 may be optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                  61
                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
40.9%; Score 128; DB 21; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                  Amino acid polymer seq ID NO: 64 of US5994109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 3..100
                                                                                                                                                                              AAY59044 standard, peptide, 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0460890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
                                                                                                                                                                                                                                                  07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference 3.
                                                     57 AAAKEAA 63
                                                                                      62 AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5994109-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                               AAY59044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                            AAY59044
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Gaps

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4,
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                                                                                                                                                                                                                                                                                                                         Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              3..100
/note= "Lys-Ala in positions 3-100 may be present or
absent"
                                                              1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sparrow J;
                16; Indels
                                                                                                                                                                                                                                                                                             Poly-Lys-Ala used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128; DB 22;
Pred. No. 9.3e-06;
5; Mismatches 16;
 Pred. No. 9.3e-06;
                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 131; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                        AAU04289 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE
62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 40.9%;
1 Similarity 62.7%;
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0462040.
                                                                                                                                                                                                                                                                  (first entry)
                  42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-365933/38.
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA;
                                                                                                                                  AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                     57 AAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1993;
                                                                                                                                                                                                                                                                  23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
                                                                                                                                  62
                Matches
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, appliepproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, drugs, oncogenes, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                         Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                         growth factor; clotting factor; apolipoprotein; receptor; drug; on tumor antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                      Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128; DB 22;
Pred. No. 9.3e-06;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cristiano RJ,
AAB45852 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.9%;
                                                                                                                                                                                                                                                                                                                                                                                         92US-0855389.
                                                                                                                                                                                                                                                                                                                                     95US-0460971.
                                                                                                                                                                                                                                                                                                                                                                      93US-0167641.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 62.7 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 AA;
                                                                                                                                                                                            bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAKEAA 63
                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1993;
                                                                     21-MAR-2001
                                                                                                                                                                                                                                                                US6150168-A.
                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1993;
                                                                                                                                                                                                                                                                                                   21-NOV-2000.
                                    AAB45852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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Matches
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16; Indels

Local Similarity

Matches

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Query Match

Length 100;

1 AKKYAK-KEKAYAKAK-KABAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56

62 AKAKAKA 68

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88 AEKAKAAYK 96

(first entry)

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1 AKKYAKKEKAYAKAKKAEAKAAKKAK-AEAKKYAAKAAKAEKKEYAA--AEAKYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                            28 AEKAEKAAEKAAEKKAKEAKKAEKAKEAEKAKEAEKAKAKAKAKAKAKAKEKAKA 87
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.1%;
Matches 38; Conservative
                                                                                                                                                                              immunological activity
                                                                                                                          (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                  certain amino acids.
                                                                                                                                                 WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                   106 AA;
                                                                                                                                                                                                                                                                                                         See also AAQ05664
                                                                                                                                                                                                                                                                                                                                                                            58 AAK-EAAYE 65
                                                                                                                                                      N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                 fusion protein.
                                                                                              16-FEB-1990;
                                                                                                         07-FEB-1990;
17-FEB-1989;
                03-JAN-1991
                                                                                   22-AUG-1990.
                                                                       EP383620-A.
                                                            Synthetic.
     AAR06446;
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                     Cook KS;
                                                                                                                                                                                                                                                                                                                              Query Match
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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrod; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidanemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                         Copolymer; molecular weight marker; TV-marker; immune disease;
                                      AAY82572 standard; peptide; 45 AA.
                                                                                                                       28-JUL-2000
                                                                                AAY82572;
RESULT 12
                                                              To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A. and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the S' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, EKA, KRA, YEA, ARA KRA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control edemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 122; DB 11; Length 106; 55.1%; Pred. No. 3.9e-05; ive 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing genes encoding random polymers of aminoacid(s) - iproducing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                Recombinant copolymer 1-19, myelin basic protein analogue.
                                    AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                90EP-0301700
                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-0473845.
89US-0312541.
                                                                                                                    (first entry)
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-acediated or mithody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chonic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                    99WO-US22402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 AA;
                                                                                                                                                                                          WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gad A, Lis D;
                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1998;
                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                       06-APR-2000.
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38.5%; Score 120.5; DB 21; Length 45;

Query Match

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4; Gaps

us-09-816-989a-4.open.rag

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins capteseed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are also useful for sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Manner and Alley Companisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Bonand JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                      Gaps
                                                                                                                                                                                                                                                                                                                                                    Antibacterial; gene therapy, vaccine, biosynthesis, biodegradation, vitamin B12, bacterial infection; disease.
                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 239;
                      6; Indels
                                                                                29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA
  71.1%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 111.5; DB Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID No 1828; 192pp; French.
                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes protein #1827
                                                                                                                                                                                            ABB49123 standard; Protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                           (first entry)
                  32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-010914/01.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOSS H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177335-A2.
                                                                                                                                                                                                                                                                         05-FEB-2002
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                                                                                                                                                                                                                                    ABB49123;
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                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used idiagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKK---EKAYAKAKAEAKA-AKKA--KAEAKKYAKAAKAEKKEYAAA------ 46
                                                                                                                                                                                                                                                                                                        Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1;
                           1 AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKY----AKAAKAEKKEYAAAEAKYKAEAAK
                                                                                                                                                                                                                                                                                                                     MDP1; slow growing acid-fast bacterium protein; immunogenicity; pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC; Mycobacterium avium intracellular complex; Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.3%; Score 110.5; DB 21; Length
47.0%; Pred. No. 0.0011;
tive 5; Mismatches 22; Indels
17; Indels
                                                                                                                                                                                                                                                                           Mycobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
13; Mismatches
                                                                                                                                                                                       AAB20575 standard; Protein; 205 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2A; 62pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2000; 2000WO-JP00455.
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                                                                                                                                                                                                                                              (first entry)
32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YAMA/) YAMADA T. (MATS/) MATSUMOTO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-543393/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis
                                                                                                    |||::|| |
163 AAEKAAAE 171
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                                                                                    AAAKEAAYE 65
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                                                                                                                                                                                                                   AAB20575;
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Matches
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comptises: (a) an oligo-dT primer and an oligouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence of the sequence of the sequence of the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the full-length
cDNAs easily without any specialised methods. AAH0366 to AAH13628 and
AAH13633 to AAH13629 to AAH13632
represent uluman amino acid sequences; and AAH13629 to AAH13632
represent charaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.7%; Score 108.5; DB 22; Length 198; 50.7%; Pred. No. 0.0016; tive 9; Mismatches 17; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hikawa T, Hayashi K, Saito K, Ye
Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 18049; 2537pp + CD ROM; English.
                                                                                                                                                      Human protein sequence SEQ ID NO:18049.
                                    AAB95499 standard; Protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota T, Isogai T, Nishikawa T,
Ishii S, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length cDNAs -
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                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                26-JUN-2001
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                                                                          AAB95499;
RESULT 15
                  AAB95499
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Yamamoto J;

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Gaps

Conservative

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52 AEAAKAAAKEA 62
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77 AKAVRAKAKVA 87
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completed: March 10, 2003, 12:21:29 ne : 34.3924 secs Search co

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GenCore version 5.1.3
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protein search, using sw model OM protein

March 10, 2003, 12:26:10 ; Search time 19.6329 Seconds
 (without alignments)
141.764 Million cell updates/sec Run on:

US-09-816-989A-4 313 Title: Perfect score:

Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

188354 seqs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

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11: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
12: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\* /grnz //prodata/1/pubpaa/US09 PUBCOMB.pep:\*
/cgnz 6/ptodata/1/pubpaa/US10 NEW PUB.pep:\*
/cgnz 6/ptodata/1/pubpaa/US10 PUBCOMB.pep:\*
/cgnz 6/ptodata/1/pubpaa/US60 NEW PUB.pep:\*
/cgnz 6/ptodata/1/pubpaa/US60 NEW PUB.pep:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		dР				
Result No.	Score	Query Match	Query Match Length DB	DB	at a	Description
	313	100.0	99	101	US-09-816-989A-4	Segmence 4. Appli
8	282.5	90.3	77	10	US-09-816-989A-5	
m	268	85.6	86	10	US-09-816-989A-6	
4	228.5	73.0	109	10	US-09-816-989A-7	
S	198	63.3		10	US-09-816-989A-3	٠.
Q	120.5	38.5	45	10	US-09-816-989A-2	
7	117.5	37.5		σ	US-09-820-843A-8	Sequence 8, Appli
80	114	36.4		σ	US-10-184-832-5	Sequence 5, Appli
6	105.5	33.7		10	US-09-816-989A-1	Sequence 1. Appli
10	104.5	33.4	223	σ	US-10-051-643-201	Sequence 201, App
11	101	32.3		10	US-09-815-242-11216	Sequence 11216. A
12	97.5	31.2		0	US-09-820-843A-27	Sequence 27, Appl
13	95	30.4		10	US-09-864-761-36182	Sequence 36182, A
14	93.5	29.9		0	US-09-882-774-1	Sequence 1, Appli
15	92.5	29.6		σ	US-09-820-843A-24	Sequence 24, Appl
16	88.5	28.3		δ	US-09-820-843A-95	Sequence 95, Appl
17	87	27.8		10	US-09-864-761-37061	Sequence 37061, A
18	85.5	27.3	80	10	US-09-815-242-5198	Sequence 5198, Ap
19	85	27.2	892	10	US-09-815-242-13765	Semience 13765. A

Sequence 90, Appl Sequence 48, Appl Sequence 10314, Ap Sequence 1164, Ap Sequence 5197, Ap Sequence 3, Appli Sequence 559, Appl Sequence 559, Appl Sequence 11, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 100, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli	Sequence 18, Appl Sequence 18, Appl Sequence 10575, A Sequence 46, Appl Sequence 7, Appli Sequence 77, Appli Sequence 571, Appli Sequence 60, Appli Sequence 251, Appli Sequence 257, Appli
9 US-09-999-724-90 9 US-09-999-724-48 10 US-09-915-242-10314 10 US-09-925-300-1164 9 US-09-738-626-5197 10 US-09-233-304-2 10 US-09-233-304-2 10 US-09-233-304-2 10 US-09-925-59 9 US-10-093-892-5 10 US-09-893-238-11 10 US-09-893-238-11 10 US-09-893-238-11 10 US-09-893-238-11 10 US-09-893-238-11 10 US-09-893-238-11 10 US-09-893-28-11 10 US-09-893-28-11	10 US-09-864-761-35241 10 US-09-876-889-18 10 US-09-815-242-10575 10 US-09-815-242-4893 9 US-09-999-724-46 9 US-09-999-724-46 9 US-10-093-892-7 10 US-09-764-846-233 10 US-09-764-846-257 10 US-09-764-846-257
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## ALIGNMENTS

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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doxis
TITLE OF INVENTION: COCOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
PILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 02/09/816,989A
CURRENT FILING DATE: 2004-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR RILING DATE: 1999-09-34
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 313; DB 10; Best Local Similarity 100.0%; Pred. No. 4e-23; Matches 66; Conservative 0; Mismatches 0;
                    Sequence 4, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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JS-09-816-989A-4
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; Sequence 5, Application US/09816989A

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Sequence 7, Application US/09816989A
| Sequence 7, Application US/09816989A
| Patent No. US20020115103A1
| GENERAL INFORMATION:
| APPLICANT: Cig. Doris
| TITLE OF INVENTION: COPCLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE;
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| FILE REFERENCE: 2609/60807-A-PCT-US
| CURRENT PILING DATE: 2001-03-23
| PRIOR FILING DATE: 1998-09-25
| PRIOR PILING DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: PATENT OF THE PATENT OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lis, Doris
TITLE OF INVENTION: COPCLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA:
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION UNDERS: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARES: PARCENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
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80.3%; Pred. No. 1.6e-12;
tive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.0%; Score 228.5; DB 1 Best Local Similarity 56.9%; Pred. No. 4.7e-15; Matches 62; Conservative 0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 80.3
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-816-989A-3
                                                                                                                                                                         US-09-816-989A-7
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Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TILLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 1098-09-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1999-09-24
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAK-----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 90.3%; Score 282.5; DB 10; Length 77; Similarity 84.4%; Pred. No. 3.2e-20; 65; Conservative 0; Mismatches 1; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 86;
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Best Local Similarity 75.6%; Pred. No. 7.9e-19;
Matches 65; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YKMEAAKKAYKAEAAKAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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US-09-816-989A-6
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Matches
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Sequence 1, Application US/09816989A

Sequence 1, Application US/09816989A

Sequence 1, Application US/0981698A

Sequence 1, Application US/0981698A

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPCLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKS

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT PILING DATE: 2001-03-23

PRIOR PILING DATE: 1998-09-25

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 35
                                                                                                                                                                                                                                                ## Sequence 5, Application US/10184832

| Sequence 5, Application US/10184832
| Sequence 5, Application No. 220030022857A1
| Sequence 5, Application No. 220030022857A1
| GENERAL INFORMATION: COMPOSITIONS AND METHODS FOR THE | TITLE OF INVENTION: COMPOSITIONS AND WEIGHT DISORDERS, INCLUDING OBESITY | TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY | FILE REFERENCE: MPI2001-056P1NM | CURRENT FILING DATE: 2002-06-28 | PRIOR APPLICATION NUMBER: 0002-06-28 | PRIOR APPLICATION NUMBER: 0003-06-28 | NUMBER OF SEQ ID NOS: 6 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NOS: 6 | SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKE-----KAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KAKAAEAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.4%; Score 114; DB 9; Length 452; 56.5%; Pred. No. 0.00087; tive 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
33.7%; Score 105.5; DB 10
Best Local Similarity 43.9%; Pred. No. 0.00037;
Matches 29; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Matches 39; Conservative
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                                                                                                          228 AEAKAATEAKRKA 240
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US-10-184-832-5
                                         54 AAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 AEAKAEAKE 166
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APPLICANT: Council of Scientific and Industrial Research
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION UNDER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 372;
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CHER INFORMATION: outer membrane integrity protein (tolA)

NAME/KEY: misc_feature

OTHER INFORMATION: gi|1573353

US-09-820-843A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lis, Doris
TITLE OF INVENTION: COPCLYMER I RELATED POLYPEP
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
SOFTWARE: PALENTIN VETSION 3.1
SQCTWARE: PALENTIN VETSION 3.1
SQCTWARE: PALENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09816989A
; Patent No. US20020115103A1
; BENERAL INFORMATION:
; APPLICANT: Gad, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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ORGANISM: H. influenzae
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                                                                    61 EAAYEA 66
                                                                                                                                         51 EAAYEA 56
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US-09-816-989A-2
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                                                                                                                                                                                                                                  APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory;
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REPERENCE: 1000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
FRICR APPLICATION NUMBER: US/9/156,181
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-112-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FRASESEQ for Windows Version 3.0
SECTION 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>6</u>
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APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: And H. Howard
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                  ; Sequence 201, Application US/10051643; Publication No. US20020197265A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-201
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52.2%;
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175 PAKKAATKA 183
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EAAYEA 66
                                             EAAYEA 35
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Sequence 27, Application US/08820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USFFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: PATENTING DATE: 2001-03-30
SOFTWARE: PATENTING DATE: 2001-03-30
SOFTWARE: PATENTING DATE: 2001-03-30
SOFTWARE: PATENTING DATE: 2001-03-30
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US-09-864-761-36182

Sequence 36182, Application US/09864761

Patent No. US20020048763A1

Patent No. US20020048763A1

APPLICANT: Penn, Sharron G.

APPLICANT: Pank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11216
LENGTH: 829
TYPE: PT
TYPE: PT
ORGANISM: Haemophilus influenzae
US-09-815-242-11216
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CTHER INFORMATION: tola protein
NAME/KEY: misc feature
CTHER INFORMATION: gi|9656364
US-09-820-843A-27
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TYPE: PRT
ORGANISM: Vibrio cholerae
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Best Local Similarity
Matches 23; Conserva
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129 KAEEQA 134
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US-09-820-843A-27
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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INPECTIVES
FITLE OF INVENTION: USEFUL AS ANTI-INPECTIVES
FILE REPRENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 24
                                                                                      : Use of Coiled-Coil Structural Scaffold to Generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AKKEKAYAKAKKAEAKAAKAKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA--KAAAKE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;
OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF;
NAME/KEY: misc_feature
;
OTHER INFORMATION: gi|9951352
US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 619;
                                                                29.9%; Score 93.5; DB 9;
45.8%; Pred. No. 0.096;
tive 11; Mismatches 18;
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Publication No. US20030039963A1
GENERAL INFORMATION:
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; ORGANISM: Streptococcus pneumoniae
US-09-882-774-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                              Michael E.
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Matches 27; Conservative
                                                             Hodges
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US-09-820-843A-24
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PARILY, SIGNAL = 1.3
OTHER INFORMATION: SWISSEROT HIT: P12036, EVALUE 2.00e-22
OTHER INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
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SEQ ID NO 36182
LENGTH: 617
                                                                      PRIOR APPLICATION NUMBER: US 50/180/312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-01-30
PRIOR PELING DATE: 2001-01-30
CURRENT APPLICATION NUMBER: US/09/864,761
                                                    APPLICATION NUMBER: US 60/180,312
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Best Local Similarity 41.6
Matches 32; Conservative
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Query Match 29.6%; Score 92.5; DB 9; Length 309; Best Local Similarity 47.8%; Pred. No. 0.058; Matches 32; Conservative 2; Mismatches 32; Indels
                                                                                                                                                                                                                                                                            Search completed: March 10, 2003, 12:53:43 Job time : 19.7758 secs
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; Sequence 1, Application US/09882774 ; Publication No. US20030021795A1

RESULT 14 US-09-882-774-1

173 AEVKSPEKAKSPAKEEA 189

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                                                                                                                                                             1 AKKYAKKEKAYAKAKKAEAK..........EAKYKAEAAKAAAKEAAYEA 66
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Sequence 5
Sequence 2
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-09-913-008A-5

US-09-913-008A-5

US-09-913-008A-5

US-09-913-684-2

US-08-293-284A-2

US-08-293-284A-2

US-08-216-894-2

US-08-216-894-2

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Maximum Match 100%
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Maximum DB seq length: 200000000
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US-08-468-985-2
US-08-312-949-2
US-08-072-070-2
US-08-469-434-2
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US-08-468-718-2
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#### ALIGNMENTS

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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
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Patent No. 6150168

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be CTHER INFORMATION: present or absent.

US-08-460-971A-64
                                                               Score 128; DB 3; Length 100;
Pred. No. 4.9e-06;
5; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: BESCHARL
SOFTWARE: FASEESE (FOR WINDOWS 2.0
SOFTWARE: FASEESE (FOR WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: UNDER: 08/167,641
FILING APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/167,641
FILING DATE: MACCH 19,1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MACCH 19,1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MACCH 19,1993
ATTORNEY,AGENT INFORMATION:
NAME: WARDLEY, RICHARD J.
REGISTRATION NUMBER: 32,32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELEFRONS: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                               Query Match
Best Local Similarity 62.7%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 100 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                        62 AKAKAKA 68
                                                                                                                                                                                                                                                                                                            57 AAAKEAA 63
      US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-460-971A-64
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                                                                                                                                                                                                                                                                                                                                                                            Sequence (4) Application US/08167641C
Patent No. 6033881
Patent Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Gattchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS STREET: Solve Lyon & Lyon
STREET: Solve Lyon
STREET: Solve
                                                                                     OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER WIFORMATION: present or absent.
                                                                                                                                                                                                             Query Match

40.9%; Score 128; DB 2; Length 100;
Best Local Similarity 62.7%; Pred. No. 4.9e-06;
Matches 42; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AKAKAKA 68
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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                                                         9 КАУАКАК-КАБАКААККАКАБАККҮАКА-АКАЕККЕУАААБАКҮКАБА-АКАААК 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION DATE: 08/08/32,436
FILING DATE: 18-DEC-1996
ATONNEY/AGENT INFORMATION:
NAME: SALLIVAN, SALLY
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.5%; Score 117.5; DB 4; Best Local Similarity 65.5%; Pred. No. 2.8e-05; Matches 36; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08993008A; Patent No. 6153596; GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Merv, Shiow-Jyi
APPLICANT: Rarr, Joan R.
APPLICANT: Rarr, Joan R.
APPLICANT: Roll, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Greenlee, Winner and Sullivan STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08993008A; Patent No. 6153596; GENERAL INFORMATION: APPLICANT: Liotta, Dennis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 303-452 ...
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                             57 AAAKEAA 63
                                                                                                                                                                                                             62 AKAKAKA 68
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US-08-993-008A-6
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                                                                                                             1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
                                                         Gaps
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                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64, Application US/08462040
Fatent No. 617754
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gritchank, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: California
CCITY: Los Angeles
STATE: California
CCUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-462-040-64
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62.7%; Pred. No. 4.9e-06;
iive 5; Mismatches 16; Indels
                                                      16; Indels
est Local Similarity 62.7%; Pred. No. 4.9e-06;
Matches 42; Conservative 5; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUMTURE READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: BEACAGE COMPUTER: JUNE P.C. DOS 5.0 SOFTWARE: JUNE S. 1995 CLASSIFICATION DATE: JUNE S. 1995 CLASSIFICATION DATE: BEACAGE TH, 1993 APPLICATION NUMBER: 07/855,389 FILING DATE: MARCH 20, 1992 APPLICATION NUMBER: PCT/US93/02725 FILING DATE: MARCH 19, 1993 ATTORNEY AGENT INFORMATION:

NANNE: WASHING THE WASHING T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212/078
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/0
TELECOMUNICATION INFORMATION:
TELEPAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELERX: (7-31)
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                       57 AAAKEAA 63
                                                                                                                                                                                                                                                                                                    62 AKAKAKA 68
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111 AKKVAKKAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKVTK 170
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IGENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Adams, John H

APPLICANT: Rappe, Stefan

TITLE OF INVENTION: Vaccine Compositions

TITLE OF INVENTION: Vaccine Compositions

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Barnes & Thornburg

STREET: 11 S Meridian

CITY: Indianapolis

STATE: Indianapolis

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/929,329
                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106; DB 3;
Pred. No. 0.0014;
5; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 AVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CAMDDEL1, CARINTYN ARGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICALL.
FILING DATE:
CLASSIFTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 8359
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-745
TELEPAX: (317) 231-745
; TELEPAX: (317) 231-745
; TELEPAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.9
Query Match
Best Local Similarity 42.4
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46204
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Patent No. 603384
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cchavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: BOJOLS

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33.95
TELEPHONE: 303-499-8089
TELEPHONE: 303-499-8089
TELEFAK: SOB OFFICE TO AND OFFICE TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                             TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                       ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 303-499-8065
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
                     Wey, Shiow-Jyi
Karr, Joan F.
Pohl, Jan
Petros, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.6<sup>3</sup>
Matches 31; Conservative
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STATE: California
COUNTRY: USA
ZÉP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                 STREET: 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: not MOLECULE TYPE: | HYPOTHETICAL: N
                                                                                                                                                                                                                                                                      STATE: CC
COUNTRY: US
CONTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
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STREET: 43
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                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-889-27
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; Sequence 2, Application US/08346849; Patent No. 5670483; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium vaccae
                                                        Query Match
Best Local Similarity 52.23
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.4
Best Local Similarity 52.2
Matches 36; Conservative
   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|| :|
175 PAKKAATKA 183
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       US-09-095-855-201
                                                                                                                                                                                                                                                                                                                    JS-09-205-426-201
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APPLICANT: Visser, Elizabeth
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKAKKAE----AKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA 55
                                                                                                                                                                                                     Score 105; DB 3; Length 1507;
Pred. No. 0.012;
6; Mismatches 14; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UNN-1997
APPLICATION NUMBER: 08/97,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: 10.0014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 201, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFRENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                          ANTI-SENSE: NO
RIGINAL SOURCE:
ORGANISM: Plasmodium yoelii
US-08-929-3229-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                         33.5%;
50.8%;
 1507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                   Query Match 33.5
Best Local Similarity 50.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                                           1232 KKALK 1236
                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        56 KAAAK 60
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CITY: Se
LENGTH:
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                                                                                                                1 AKKYAKKEKAYAK---AKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 57
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APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Total BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
AUTHER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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FACENTERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: WALSON, James D.

APPLICANT: WALSON, James D.

APPLICANT: WALSON, James D.

TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

FILE REFERENCE: 11000.100.2c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT APPLICATION NUMBER: 09/095,855

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER APPLICATION NUMBER: 08/97,362

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PastSEQ for Windows Version 3.0

ENGITHAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
  Length 223;
                                                        Indels
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33.4%; Score 104.5; DB 4;
52.2%; Pred. No. 0.002;
tive 4; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.4%; Score 104.5; DB 4;
52.2%; Pred. No. 0.002;
tive 4; Mismatches 20;
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Score 102.5; DB 2; Length 433;
Pred. No. 0.0061;
9; Mismatches 22; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKYAKKEK------AYAKAK-KAEAKAAKKAKAEAKKYAKAEKAEKKEYAAA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08216894

Patent No. 5876734

GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
TITLE OF INVENTION:
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STRRET: 3000 & Street, N.W., Suite 500
COTTENTION OF SECUENCES: 10
COTTENTION OF SECUENCES: 10
COTTENTION OF SEQUENCES: 10
COTTENTION OF SECUENCES: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 564;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 99,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.4%; Score 101.5;
PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 433 amino.
                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.7%;
Best Local Similarity 41.0%;
Matches 32; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 564 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-216-894-2
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APPLICANT: Holmes, Todd
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102.5; DB 1; Length 433;
Pred. No. 0.0061;
9; Mismatches 22; Indels 15
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBTRANTON DATA:
APPLICATION NUMBER: US/08/293,284A
FILING®DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive
                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERNICE/DOCKET NUMBER: MIT-6008
TELECOMUNICATION INFORMATION:
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08293284A Patent No. 5955343
                   COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 433 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 EAKYKAEAAKAAAKEAAY 64
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Best Local Similarity 41.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-346-849-2
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STATE: Massachusetts
COUNTRY: U.S.A.
             Massachusetts
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US-08-293-284A-2
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391 EAA 393
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                                                             2 KKYAKKEKAYAKAKAEAKAAKKAKAKAEAKKYAKAAKA-EKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKAKAEAKAAKAAKAEAKKYAKAAKA-EKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.4%; Score 101.5; DB 4; Length 564; Best Local Similarity 46.0%; Pred. No. 0.0099; Matches 29; Conservative 10; Mismatches 23; Indels 1.
                                                                                                                                                                                                                                                                         Sequence 2, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kitchhoff, Louis V.
APPLICANT: Cotau, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INPECTION
TITLE OF INVENTION: WITH TRYPANOSOWA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLY & Lardner
STREET: 3000 K Street, N.W., Suite 500
Best Local Similarity 46.0%; Pred. No. 0.0099;
Matches 29; Conservative 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECHOMIN: (202)672-5300
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington, D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-216-894-8
; Sequence 8, Application US/08216894
; Retent No. 5876/34
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                         61 EAA 63
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                                                                                                                                                                                                                                      RESULT 14
US-09-115-746-2
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:15:04; Search time 22.5802 Seconds (without alignments) 327.825 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-816-989A-5 366 1 AKKYAKKEKAYAKKAEKAAK......BAKYKAEAAKAAAKEAAYEA 77

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMADIES

		d			SUMMARIES	
Result No.	Score	Ouery Match	Query Match Length	BB	ΙD	Description
-	150.5		421	7	JV0057	tolA protein - Esc
8	148	40.4	394	7	F90725	membrane spanning
е	148	40.4	394	7	G85576	
4	146	39.9	376	N	AG0592	prot
5	141.5	38.7	347	N	E83525	Tola protein PA097
9	141	38.5	372	~	G64064	outer membrane int
7	138	37.7	1701	0	T09127	probable erythrocy
89	136	37.2	210	0	A25550	histone H1 - sea u
σ	m	36.7	219	7	E60110	repetitive protein
10	134.5	36.7	231	~	5958	
11	134	36.6	1128	~	T30296	R27-2 protein - Tr
12	133	36.3	328	N	A44993	cytosolic repetiti
13	130.5	35.7	388	~	AC0138	Tola colicin impor
14	130	35.5	1390	N	S51364	sperm tail-specifi
15	129.5	35.4	214	~	G70673	probable hupB - My
16	128.5	35.1	211	N	A28100	histone H1-beta, e
17	127.5	34.8	344	~	834153	mst101-1 protein -
18	127	34.7	217	N	A26721	ж,
19	123	33.6	248	Н	HSUR1P	histone H1, gonada
20	123	33.6	433	~	S25194	yea
21	122.5	33.5	206	~	509388	- 86
22	122.5	ë.	220	7	A28456	histone H1.10 - ch
23	122.5	ë	311	7	T17698	ď
24	N.	'n.	243	7	AE1689	
25	121.5	m.	239	~	AE1317	
56	٠	'n.	384	~	B43592	C
27	120.5	•	284	7	T06241	H1 (clor
28	•	32.4	241	~	JN0748	HI-II
29	118	32.2	206	Н	HSTR1R	histone H1 - rainb

56 AAEAKYKAEAAKAAKEAAYEA 77 || || || || || || || || 190 AAALKKKAEAAEAAAAEARKKA 211

δ g RESULT 2 F90725

probable translati cgcr-4 protein - C	histone H1 (clone histone H1.1L - c	hypothetical prote conserved hypothet histone H1.03 - ch	histone H1.02 - ch histone H1 - musco	outer membrane ant tolA protein VC183	histone H1 homolog histone H1.1 - Cae	histone H1.01 - ch	histone H1-5 [vali h-caldesmon - chic
T11583 S19113	T06257 B28456	T06636 E75383 D28456	HSCH1 S01262	F71283 A82152	S61926 T23778	A23055	S51660 A33430
000	200	N N N	7 7	01 01	0 0	0	н н
1403 265	288	581 581 781	218	325 356	182 208	218	226 771
32.2	32.1	31.6	30.7	30.5	30.3 30.3	30.3	30.2
		115.5 31.6 114 31.1 113.5 31.0					110.5 30.2

## ALIGNMENTS

C)Species: Escherichia coli (strain K-12) C)Species: Escherichia coli C,Species: Escherichia coli C,Species: Escherichia coli C,Species: Escherichia coli C,Saccession: 3V0057, B64810 R,Levengood, S.K.; Webster, R.E. J. Bacteriol. 171, 6600-6609, 1899 A,Title: Nucleotide sequences of the tola and tolB ge A,Reference number: JV0057, MUID:90078104; PMID:26872 A,Accession: 4V0057 A,Molecule type: DNA A,Experimental source: Strain JM105 A,Experimental source: Strain JM105 A,Experimental source: Strain JM105 A,Title: The camplete genome sequence of Escherichia A,Reference number: A64720; MUID:97426617; PMID:92785 A,Title: The complete genome sequence of Escherichia A,Reference number: A64720; MUID:97426617; PMID:92785 A,Title: The complete genome sequence of Escherichia A,Resaidues: 1421 ABLAT> A,Cross-references: GB.AE0AT> A,Gene: tolA A,Gene: to	RESULT 1 JV0057	
C; Date: 07-Sep-1990 #Sequence C; Accession: 170057; B64810	tolA protein - Escherichia coli (strain K-12) C.Species: Racherichia coli	n - n
R; Levengood, S.K.; Webster, R. J. Bacteriol. 171, 6600-6609, A; Title: Nucleotide sequences A; Reference number: JV0057; NC A; Residues: 1-421 < LEEV> A; Residues: 1-421 < LEEV> A; Cross-references: GB: M28222; A; Experimental source: strain A; Note: the authors translated B; Blattner, F.R.; Plunkett III A; Rose, D.J.; Mau, B.; Sha Science 277, 1453-1462, 1997 A; Title: The complete genome s A; Reference number: A64720; NC A; Attle: The complete genome s A; Reference number: A64720; NC A; Attle: The complete genome s A; Residues: 1-421 < BLAT> A; Cross-references: GB: AE00017 A; Estatus: nucleic acid sequenc A; Besidues: 1-421 < BLAT> A; Cross-references: GB: AE00017 A; Estatus: nucleic acid sequenc C; Genetics: A; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Keywords: nucleotide binding F; 14-34/Domain: transmembrane F; 18-34/Domain: transmembrane F; 18-34/Domain: thelical #stat F; 18-301/Domain: helical #stat F; 18-301/Domain: helical #stat Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABAKKAB	C.Accession: JV0057: R64810	Sep-
A; Title: Nucleotide sequences A; Reference number: JV0057; MU A; Residues: 1-421 <lev. 1-421="" <blat="" <lev.="" a4720;="" a;="" authors="" b.;="" bb.m38232;="" blattner,="" coss="" d.j;="" experimental="" f.r.;="" iii="" j.d.;="" j.j.;="" mau,="" mu="" note:="" number:="" plunkett="" r;="" reference="" references:="" residues:="" rose="" rose,="" shacketter="" source:="" strain="" the="" translated=""> A; Residues: 1-421 <blat> A; R</blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></blat></lev.>	Rilevengood, S.K.; Webster, R.E.	
A, Accession: JV0057, Accession: JV0057, Accession: JV0057 A, Molecule type: DNA A, Rosidues: 1-421 (-428) A, Experimental source: strain A, Experimental source: strain A, Experimental source: strain A, Experimental source: strain A, Rose, D.J.; Mau, B.; Shac Science 277, 1453-1462, 1997 A, Title: The complete genome B A, Reference number: A64720; MU A, Rocession: B64810 A, Redecession: B64810 A, Redecession: B64810 A, Rosidues: 1-421 (ABLAT) A, Cross-references: GB.AE00017 A, Experimental source: strain C, Comment: tolA and tolB prote C, Genetics: A, Genetics: A, Genetics: C, Genetics: A, Genetics: C, Genetics: A, Genetics: A, Genetics: C, Gonetics: C, Gonetics: C, Gonetics: C, Gonetics: C, Gonetics: C, Gonetics: A, Genetics: A, Genetics: C, Gonetics: C, Goneti	A) Title: Nucleotide sequences to the tola and tola genes and localization of their production of the production of the control of the contro	cleo
A; Molecule type; DNA A; Residues: 1-421 < LEV- A; Cross-references: GB.M28232; A; Experimental source: strain A; BAttner, F.R.; Plunket III. A; Rose, D.J.; Mau, B.; Shac Science 277, 1453-1462, 1997 A; Title: The complete genome B; Reference number: A64720; MU A; Reterence number: A64720; MU A; Reterence number: A64720; MU A; Residues: 1-421 & BLAT> A; Cross-references: GB.AE00017 A; Experimental source: strain C; Comment: tolA and tolB prote C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Genetics:	A; reletence number: 0,0003/; mold:900/0104; rmlD:200/24/ A; Accession: JV0057	B,
A, Gross-references: GB M28232, A, Experimental source: strain A, Note: the authors translated B, Blattner, F.R.; Plunkett III. A,; Rose, D.J.; Mau, B.; Shac Science 277, 1453-1462, 1997 A, Title: The complete genome B, Reference number: A64720; MU A, Roteus: nucleic acid sequenc A, Molecule type: DNA A, Rosidues: 1-421 ABLT> A, Experimental source: strain C, Comment: tolA and tolB prote C, Genetics: A, Genetics: B, Genetics: B, Genetics: A, Genetics: A, Genetics: A, Genetics: B, Genetics: B, Genetics: B, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: B, Genetics: B, Genetics: A, Genetics: A, Genetics: A, Genetics: B, Genetics: B, Genetics: B, Genetics: A, Genetics: B, G	A; Molecule type: DNA	type
A; Experimental source: strain A; Bote: the authors translated R; Blattner, F.R.; Plunkett III A; Rose, D.J.; Mau, B.; Shac Science 277, 1453-1462, 1997 A; Title: The complete genome B A; Reference number: A64720; MU A; Rocession: B64810 A; Roteus: nucleic acid sequenc A; Molecule type: DNA A; Rosidues: 1-421 «BLAT> A; Cross-references: GB.AE00017 A; Experimental source: strain C; Comment: tolA and tolB prote C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: A; Genetics: A; Genetics: C; Genet	A; Cercus: 1-21 LLDV; AB232; NID:q148018; PIDN:AAA24683.1; PID:q148019	eren
A,NOCE: The authors translated R,NOSE: The authors translated Science 277; Mau, B; Shac Science 277; Mau, B; Shac Science 277; 1453-1462; 1997 A;Title: The complete genome E A;Reference number: A64720; W A;Accession: B64810 A;Accession: B64810 A;Residues: 1-421 <blat> A;Residues: 1-421 <blat> A;Residues: 1-421 <blat> A;Comment: tolA and tolB prote C;Goment: tolA and tolB prote C;Gometics: A;Gone: tolA A;Map position: 17 min A;Start codon: GTG C;Keywords: nucleotide binding F;14-34/Domain: transmembrane F;78-301/Domain: helical #stat F;355-362/Region: nucleotide-F Guery Match Best Local Similarity 53; Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKA</blat></blat></blat>	A, Experimental source: strain JM105	tal
A.; Rose, D.J.; Mau, B.; Sharschence 277, 1453-1462, 1997 A;Title: The complete genome B, Reference number: A64720; NU A;Accession: B64810 A;Residues: 1-421 acid sequenc A;Comment: Lola and tols prote C;Comment: tola and tols prote C;Goment: tola A;Bap postition: 17 min A;Start codon: GTG C;Koywords: nucleotide binding F;78-301/Domain: helical #stat F;78-301/Domain: helical #stat F;355-362/Region: nucleotide-L Guery Match Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKABKAAKKA	A;Note: the authors translated the intilation codon GTG for residue 1 as Val. R.Blattner P.R.: Plunkert III. G.: Bloch C.A.: Perna. N.T.: Burland. V.: Rilev. M.:	aut. F.R
Alticle: The complete genome RA; Reference number: A64720; MU A; Reference number: A64720; MU A; Retension: B64810 A; Retension: B64810 A; Redidues: 1-421 ABLAT> A; Cross-references: GB.AE0017 A; Experimental source: strain C; Comment: tolA and tolB prote C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Geneti	.A.; Rose, D.J.; Mau, B.; Shao, Y.	D.G.
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A; Molecule type: DNA A; Residues: 1-421 < BLAT> A; Cross-references: GB: AE00017 A; Experimental source: strain C; Comment: tola and tolB prote C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Keywords: 10 min A; Eart codon: GTG C; Keywords: nucleotide binding F; 14-34 / Donmain: transmembrane F; 78-301 / Domain: belical # stat F; 355-362 / Region: nucleotide-b Query Match Query Match A1:1 Best Local Similarity 53:7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKAEKAAKKAE	A;Status: nucleic acid sequence not shown; translation not shown	ucle
A, Cross-references: GB.AE00017 A, Experimental source: strain C, Comment: tola and tola prote C, Genetics: A, Gene: tola A, Map position: 17 min A, Eart codon: GTG C; Keywords: nucleotide binding F; 14-34 / Domain: belical #stat F; 78-301 / Domain: belical #stat F; 355-362 / Region: nucleotide-b Query Match Guery Match Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKA	A MOLECULE TYPE DNA A Does dries : 2.421 cmm.	type
A; Experimental Source: Strain C; Comment: tolA and tolB prote C; Genetics: A; Gene: tolA A; Map position: 17 min A; Start codon: GTG C; Keywords: nucleotide binding F; 14-34/Domain: transmembrane F; 76-301/Domain: helical #stat F; 355-362/Region: nucleotide-F; 78-301/Domain: helical #stat F; 355-362/Region: nucleotide-F; 78-301/Pomain: helical #stat P;	A:Cross-references: GB:AE000177: GB:U00096: NID:G1786955: PIDN:AAC73833.1: PID:G1786960:	eren
C;Comment: tolA and tolB prote C;Genetics: A;Gene: tolA A;Map position: 17 min A;Start codon: GTG C;Keywords: nucleotide binding F;14-34/Domain: transmembrane F;78-301/Domain: helical #stat F;355-362/Region: nucleotide-Ł Query Match Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKRAKKO Dh 130 KOKOAFREABARKABEN	A; Experimental Bource: strain K-12, substrain MG1655	tal
C;Genetics: A;Gene: tolA A;Map position: 17 min A;Start codon: GTG C;Keywords: nuclectide binding F;14-34/Domain: transmembrane F;18-301/Domain: helical #stat F;355-362/Region: nucleotide-b Query Match Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKA	C; Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t	tolA
A;Gene: tolA A;Map position: 17 min A;Kart codon: GTG C;Keywords: nucleotide binding F;14-34/Domain: transmembrane F;78-301/Domain: helical #stat F;355-362/Region: nucleotide-b Query Match Best Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKAEKAAKKO Dh 130 KOKOAFREABARKA	C, Genetics:	
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A;Sterr Codon: GTG C;Keywords: nucleotide binding F;14-34/Domain: transmembrane F;78-301/Domain: helical #stat F;385-362/Region: nucleotide-F Guery Match Beet Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKO Dh 130 KOKOAFRAAARAABAKKA	A; Map position: 17 min	ion:
C) APPACE STATE TO THE TOTAL BY JAT 14-34/Domain: transmembrane F;78-301/Domain: transmembrane F;78-301/Domain: transmembrane F;78-301/Domain: transmembrane F;78-362/Region: nucleotide-F Guery Match Beet Local Similarity 53.7 Matches 44; Conservative Oy 3 KYAKKEKAYAKKABKAAKKA Dh 130 KOKOAFRAAARAAAKAA	A; Start Codon: GIG	: i
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P;355-362/Region: nucleotide-b Query Match Best Local Similarity 53.7 Matches 44; Conservative Qy 3 KYAKKEKAYAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAEKAAKKAAKKAEKAAKKAANAKKAEKAAKKAANAKKAAKKAANAKKAKANAKKAANAKKAANAKKAANAKKAKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKAANAKKA	F;78-301/Domain: helical #status predicted <hsr></hsr>	main
Quer 3est 4atc	F;355-362/Region: nucleotide-binding motif A (P-loop)	egio
√atc c	<pre>\$; Score 150.5; DB 2; Length 421;</pre> <pre>\$; Pred. No. 0.00019;</pre>	ch 1 Sir
		44;
		YAKK
	Db 130 KOKOABEBAAKAABADAKAKAEADAKAABEBAAKKAAADAKKKAEABAAKAAABAOKKAEAA 189	OKQAI

5.

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Nature 413, 848-852, 2001
Ajauthors: Parry, C.; Quali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajauthors: Parry, C.; Quali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajritle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; PMID:11677608
A; Status: preliminary
A; Status: preliminary
A; Status: DNA
A; Residues: 1-376 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toolard protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C.Species: Pseudomonas aeruginosa
C.Species: Deeudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: B83525
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxbig, K.; Lim, Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathox A; Reference number: A82950; MUD:20437337; PMID:10984043
A; Focession: E83525
A; Status: preliminary
A; Molecule Cype: DNA
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A; Residues: 1-347 <STO>
A; Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A; Experimental cource: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64064; UG5212
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, I. R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, I. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                         A;Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176 C;Genetics:
A;Gene: STY0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 AKKKAEAEA--AKAAADAKKKAEAEAAKAAAEAKKKAEAEAAK--AAADAKKKADAEAAK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YKAAE-A 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKK----EY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 141.5; DB 2;
Pred. No. 0.00077;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 146; DB 2;
Pred. No. 0.00038;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 КККАКАЕАККҮАКААКАЕККЕУАААЕАКУКАЕААКАААКЕАА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AAAEAKYKAEAA-----KAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.78;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.4%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 44.1
nes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: tolA; PA0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Bscherichia coli C;Species: Bscherichia coli C;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: P90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench; A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
A;Residues: 1-394 cHAx>
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Gene: ECS0774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli (C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C; Date: N.T.; Plunkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew 11-E, Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Accession: G85576
A; Accession: G85576
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <STO> A; Reperimental source: strain O157:H7, substrain EDL933
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tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
CSpecies Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;AccesBion: AG0592
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Churcher, th, T.; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                             gend
         protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                 O.O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYA----KKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 148; DB 2;
Pred. No. 0.00028;
7; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAAEAAAEARKKAAAEKAADKKAAEKA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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RiHoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.., Infect. Infmun. 57, 1959-1967, 1989
A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Reference number: A60110; MUID:89277508; PMID:2659529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-219 <HOF>
C;Comment: This protein contains a series of tandem repeats, each fourteen residues in le
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; S61122
C;Accession: S59589; S61122
C;Accession: S59589; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone genf A;Reference number: S59581; WUID:96120862; PMID:8590479
A;Accession: S59589
                                                                                         sea urchins Lytechinus pictus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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A;Cross-references: EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R. submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Trypanosoma cruzi
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ATKVAGDEKOKAABATKVAKVAEAEKORAREATKVAEAEKOKAAEATKVAEAEKOKAABA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 KTEAQKARAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYA-KAAKAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                            A,Accession: A2550
A,Molecule type: DNA
A,Residues: 1-210 <KNO.
A)Cross-references: GB:XX4488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 136; DB 2; Length 21
53.3%; Pred. No. 0.0013;
tive 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repetitive protein antigen 27 - Trypanosoma cruzi (fragments)
                                       Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the A;Reference number: A25550; MUID:87040778; PMID:3022245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histone H1 - Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.34
Matches 40; Conservative
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Matches 38; Conservative
                   R; Knowles, J.A.; Childs, G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 PAKKAÁKKPÁÁKKÁÁ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TKVÁEÁGKOKÁAEÁA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 KYKAEAAKAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: E60110
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                                       A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A;Wolecule type: DNA
A;Cross-references: GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; T
R;Sen, K.; Sikkema, D.J.; Murphy, T.F.
Gene 178, 75-81, 1996
Gene 178, 75-81, 1996
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA a A;Reference number: JC5212, MUID:97080550; PMID:8921895
A;Accession: JC5212
A;Accession: JC52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: Z16577; MUID:98115903; PMID:9448314
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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun.1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25550
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C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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A, Note: the authors translated the codon CGT for residue 190 as Ala C, Genetics:
C, Genetics:
A, Gene: tolA
A, Start codon: GTG
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A;Molecule type: DNA
A;Residues: 1-1701 .KAA>
A;Cross-references: EMBL:AF031886; NID:g2947227; PID:g2947228
A;Experimental source: subspecies yoelii; strain YM
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54.7%; Pred. No. 0.00088;
iive 7; Mismatches 20;
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Best Local Similarity
Matches 47; Conserva
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A, Gene: maebl
A, Accession:
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4; Gaps

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"TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0136 #sequence_revision 02-Nov-2001
C;Accession: AC0136 #sequence_revision N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Lil, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Drosophila hydei
Cispecies: Drosophila hydei
Cispecies: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
CiAccession: 55:1364; 534158
CiAccession: 55:1089-1095, 1994
Bur. J. Biochem. 225, 1089-1095, 1994
Alfille: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representable-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
AlReference number: 551364; MUID:95045538; PMID:7957199
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-388 «KUR»
A,Cross-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
A,Genetics:
A,Genetics:
                                                                                                                                                                               110 ATKVAEAEK---QKAAEAMKVAEAEKQKAAEATKVAEAEKQKAAEAAKAVETEKQKAAEA 166
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                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA-EKKEYAAAEA 59
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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Pred. No. 0.015;
                     22; Indels
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                     9; Mismatches
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51.7%;
                     Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                         60 KYKAEAAKAAAKEA 73
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214 VEVAEKAAADAA 225
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A; Description: The organization, structure and controlling elements of Chlamydomonas his A; Reference number: $62122
A; Reference number: $62122
A; Accession: $62122
A; Colecule 1-ype: DMA
A; Residues: 1-73, 'P', 174-231 < FAW>
A; Cross-references: EMBL:U16726; NID:9571479; PIDN:AAA98452.1; PID:9571480
C; Genetics:
A; Introns: 62/3; 101/3
C; Superfamily: histone H1
C; Reywords: chromosomal protein; DNA binding; nucleosome
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CiSpecies Trypanosoma cruzi

CiSpecies Trypanosoma cruzi

CiDate: 14-May-1993 #sequence_revision 14-May-1993 #text_change 02-Jun-2000

CiAccession: A44993

Mol. Biochem. Parssitol: 35, 127-136, 1989

A/Title: Structure and expression of two Trypanosoma cruzi genes encoding antigenic prot A/Accession: A44993

A/Accession: A44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.7%; Score 134.5; DB 2; Length 231; Best Local Similarity 47.3%; Pred. No. 0.0018; Matches 44; Conservative 4; Mismatches 26; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.6%; Score 134; DB 2; Length 1128; Best Local Similarity 52.0%; Pred. No. 0.0067; Matches 39; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 328;
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Pred. No. 0.0031;
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Best Local Similarity
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Gaps

2

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16; Gaps

23; Indels

3; Mismatches

45; Conservative

Matches

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probable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17--Ual-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70673
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, V.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Accession: G70673
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: GB:Z83018; GB:AL123456; NID:93261671; PIDN:CAB05427.1; PID:g1694845
A;Genetimental source: strain H37Rv
C;Genetics: A;Gene: hupB
C;Superfamily: histone H1
                                                                                                   Query Match 35.4%; Score 129.5; DB 2; Length 214; Best Local Similarity 45.7%; Pred. No. 0.004; Matches 43; Conservative 4; Mismatches 28; Indels 19; Gaps
2 KKYAKKEK--AYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAK----AE 50
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| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 KKKCEKAAKERKEAAEKKKCEEAAKKE 597
                                                                                                                                                                                                                                                                                                                                               51 KK--EYAAAEAKYKAEAAK---AAAKE 72
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GenCore version 5.1.3
Copyright (c) 1993 ~ 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 17.5443 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-816-989A-5 366 1 AKKYAKKEKAYAKKAEKAAK........EAKYKAEAAKAAAKEAAYEA 77

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P19934 escherichia P50600 pseudomonas P44678 haemophilus P06144 lytechinus P06144 lytechinus P50619 mycobacteri 008696 drosophila P95109 mycobacteri 008695 drosophila P07796 strongyloce P15869 strongyloce P2750 treponema P40270 tricnomus P40270 chironomus P40276 chironomus P40266 glyptotendi P08287 gallus gall P09287 gallus gall P09287 gallus gall P09426 anas platyr P19649 treponema p P19649 treponema p
SUMMARIES	TOLA ECOLI TOLA ECOLI TOLA PERAE H1 LYTP1 DBH MYCHO TREADAL ALE STRPU H1B STRPU H1D CHICK TWBB TREADH H1D CHICK H1D
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Length	205 205 210 210 210 210 210 210 210 210 210 210
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Score	141 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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H101_CHICK H15_HUMAN CALD_CHICK H11_GLYBA H11_GLYBA H1A_CHITE H1A_CHITE IF2_PASMU H11R_CHICK H16_CHICK H16_CHICK H16_CHICK H16_CHICK H16_CHICK H16_CHICK	
218 225 225 233 232 232 218 218 219	
88888888888888888888888888888888888888	
111 110.5 110.5 110.5 109.5 109.5 108 107.5 106.5 105.5	
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# ALIGNMENTS

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MEDLINE=97113525; PubMed=8955385;
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TOLA HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                           MEDLINE=99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plucekthun A., Wlodawer A.;
With its coreceptor, the C-terminal domain of Tola.";
Structure 7.711-72(1999).
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A
COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE
COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
OF BACTERIOPHAGE DNA.
-!- SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAK-----AAKAEKK-EYA 55
                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                               AND LAMB.
SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
        "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 150.5; DB 1; Length 421; 53.7%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   (2,4).
8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                     EMBL; M28232; AAA24683.1; -.
EMBL; AE000177; AAC73833.1; -
                                                                                                                                                                                                                                                                                                                                                            EMBL; D90713; BAA35405.1; -. PIR; JV0057; JV0057.
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421
310
421
278
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TOLA OR PA0971.
Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                          PIR; JV0057;
PDB; 1TOL; 2
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Indels 29; Gaps
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=204373737; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004530; AAG04360.1, -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKA----YKAAE-A 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Dennis J.J., Lafontaine B.R., Sokol P.A.; "Identification and characterization of the tolQRA genes of
                                                                                                                                                               Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 347 PEKALFARANIA
209 216 POLY-ALA.
347 AA; 37935 MW; BEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PERIPLASMIC (POTENTIAL).
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 KKKAAEEAKKKA-AAEAAKKKAAVEAAKKKAAAAAAARKAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 KKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 141.5; DB 1
Pred. No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOLA HAEIN STANDARD; PRT; 372 AA. P44678; P94810; 01-NOV-1995 (Rel. 32, Created) 15-UNOV-1995 (Rel. 32, Last sequence update) 15-UNOV-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%; Pred. No.
                                                       Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                     REVISIONS TO N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
37
347
216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
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TOLA OR HI0383.
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DBH_MYCBO
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                                                                                                                                                Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AKRLAAAAKQAEEEAKAKAAEIAAQKAKQEAEAKAKLEAEAKAKAVAEAK--AK-AEAEA 214
STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95550630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYA-----KKEKAYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAKAEK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !ransport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                     Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K -> R (IN STRAIN 1479).
A -> P (IN STRAIN 1479).
A -> P (IN STRAIN 1479).
A -> A (IN STRAIN 1479).
D -> A (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
T -> F (IN STRAIN 1479).
L -> F (IN STRAIN 1479).
I -> V (IN STRAIN 1479).
I -> V (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
                                                                                                                                                                                                                                                                                           -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
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-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
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54.7%; Pred. No. 0.00049;
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PERIPLASMIC
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                                                                                                                                                                                                                             MEDLINE=97080550; PubMed=8921895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32722; AAC22041.1; -.
EMBL; U32470; AAC44596.1; -.
HSSP; P19934; ITOL.
                                                                                                                                                                          Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 3
372 AA;
                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
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                                                                                                                                                                                                                  STRAIN=1479
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SEQUENCE
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RESULT 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYA-KAAKAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                  Knowless J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins
"Comparison of the late H1 histone genes of the sea urchins
Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8131(1986).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELIULAR LOCATION: NUCLear.
-!- SUBCELIULAR LOCATION: UNCLear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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09XB18; 09S5J5;
16-0CT-201 (Rel. 40, Created)
16-0CT-201 (Rel. 40, Last sequence update)
16-0CT-201 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
Mycobacterium boyis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%; Score 136; DB 1;
53.3%; Pred. No. 0.00072;
iive 7; Mismatches 26;
                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhīst_N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87040778; PubMed=3022245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04488; CAA28177.1; -.
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156 PAKKAAKKPAAKKAA 170
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A25550; A25550.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=ANS;
                                                                                                                                                                                                                                                                        NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1765;
                                                                                                                                        Late histone H1
                                                                                                                                                                                                                                                                                                                                                          IISSUE=Embryo;
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                                                                                                                                                                                                                                           Lytechinus
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAVKATKSPAKKVTKAVKKTAV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mstl01(2).
MST101(2).
Drosophila hydei (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
11 TaxID=7224;
Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAAKKA--EAKAYKAA-----EAKKKAKAKAKAKAAKAEKK 52
                                                                                                                                    Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth
from Mycobacterium.";
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MEDLINE=95045538; PubMed=7957139;
Neesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 35.5%; Score 130; DB 1; Length 205; Local Similarity 49.4%; Pred. No. 0.0019; tes 42; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 205 DEGENERATE REPEATS REGION 199 199 A -> T (IN REF. 2). 205 AA; 21262 MW; 19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00216; Bac DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; I.
PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P02346; 1HUU.
InterPro, IPR000119; Bac_DNAbind.
InterPro, IPR001386; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB013441; BAA78330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y18421; CAB46493.1;
                                                                                                                     STRAIN=BCG / Tokyo;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MST2_DRC
Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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1D MST2_DROHY
1D MST2_DROHY
1D 01-FEB
DT 10-FEB
DT 10-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DEMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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MEDLINE=9825987, PubMed=9634230;
MEDLINE=9825987, PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holrcyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKYAKKEK--AYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAK----AE
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                                                                                                          Drosophila hydei.";

Bur. J. Biochem. 225:1089-1095(1994).

-I. FUNCTION: POSSIBLE STRUCTURAL IN THE SPERM TAIL.

-I. SUBCELLULAR LOCATION: Cycoplasmic.

-I. SUBCELLULAR LOCATION: Cycoplasmic.

-I. TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 130; DB 1; Length 1391; 51.7%; Pred. No. 0.0087; cive 3; Mismatches 23; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA.
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us-09-816-989a-5.open.rsp

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SEQUENCE FROM N.A.
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SO THE SOCIOUS CONTRACTOR SOCIOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                 Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J., BoBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Savita P.,
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
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                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and
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45.7%; Pred. No. 0.0021;
tive 4; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37Rv;
Pragad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z83018; CABO5427.1; -.
EMBL; AE007127; AAK47393.1; -
HSSP; P02346; 1HUU.
STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 45.7
43; Conservative
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Q9ZHCS;
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AC Q92ZIC
DT 16-OC
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DT 16-OC
DT 16-OC
DE DNA-D
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OS MYCOD
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OC Actin
OX (1)
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"The Drosophila hydei gene Dhmstlol(1) encodes a testis-specific,
"The Drosophila hydei gene Dhmstlol(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant files.";
Dev. Biol. 162:414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: CYCOPIAGMIC (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
                                                                                                                                                                                             smegmatis.";
Mol. Gen. Genet. 260:475-479(1998).
Mol. Gen. Genet. 260:475-479(1998).
-! FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AKKAAKKAPAKKAAAKKTATKAAAKKAPAKKAATKAPAKKAATKAPAKKAATKAPAKK-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MST101(1).
Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK---EKAYAKK--AEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEKKE 53
                                                                                                 Lee B.H., Murugasu-Oei B., Dick T.; "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIAL HISTONE-LIKE DOMAIN.
DEGENERATE REPEATS REGION.
CASFS77F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.2%; Score 129; DB 1;
Best Local Similarity 52.4%; Pred. No. 0.0023;
Matches 44; Conservative 6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF068138; AAD13809.1; -.
HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac DNAbind.
Pfam; PF00216; Bac DNA bInding; 1.
Propu; PD000945; Bac DNAbind; 1.
SNART; SM0041; BHL: 1.
STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 -ААТКАРАККАААКАРАККААТКА 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 YAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 208 AA; 21230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MST1_DROHY
1D MST11_D
CORRESPOND
DT 01-FEB
DT
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ProDom; PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                             H1B_STRPU
P15869;
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iab.sib.ch).
                                                                                                                                                                                   EMIDIO, 503-153; 534153.

PIR; 534153; 534153.

PIR; 534153; 534153.

Sperm; Repeat; Multigene family.

DOMAIN 58 337 16 AA APPROXIMATE TANDEM REPEATS OF R-K-K-C-X-E-X-A-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                 81 AKK--EKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEK 138
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAK--AEAKKYAKAKKE----- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87172742; PubMed=3031476; Median 27., Childs G.7.; Childs G.7.; Laids Lion, characterization, and expression of the gene encoding that histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 7:478-485 (1987).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL. POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                              DB 1; Length 344;
                                                                                                                                                                                                                                                                                           Score 127.5; DB 1; Length 3 Pred. No. 0.0043; 6; Mismatches 23; Indels
                                                                                                                                                                                                                                                  K-K-C-X-B-X-A-[KQ]-K-X-)
24C65D2510387E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          139 KKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEA 176
                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Histore H1-gamma, late.
                                                                                                                                                                                                                                                                                                                                                                                                               -----KKEYAAAEAKYKAEAAK----AAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inčerpro; IPR001386; Histone H1/H5.
Interpro; IPR003216; Linkerhīst_N.
Pfam; PR00538; linker_histone; Ī.
                                                                                                                                                                                                                                                                  344 AA; 37793 MW;
                                                                                                                                                                             EMBL; X73480; CAA51875.1; -.
                                                                                                                                                                                                                                                                                             34.8%;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
    SPERMATID BUNDLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A26721; A26721.
HS&P; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purpuratus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRPU
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H1G STRE
P07796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                       'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINES 88246461; PubMed=2837660;
MEDLINES 88246461; PubMed=2837660;
Liai Z.-C., Childs G.;
"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urchin Strongylocentrotus purpuratus.";
Strongylocentrotus purpuratus.";
-I-FUNCTION: H1STONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-I-SUBCELLULAR LOCATION: Nuclear.
-I-SIMILARITY: BELONGS TO THE H1STONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 KSDAQKAPDAAKKAKLAAKKKEAKEKKAARKKEKLAAKKASKKTTKKVKKPAAKKAK 155
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                 2 KKYAKKEKAYAKKAEK------AAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Gaps
Productive accounts of the protein; DNA-binding; Multigene family. Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein, Nuclear protein, DNA-binding, Multigene family. SEQUENCE 211 AA; 22169 MM; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAK------AAKAEK 51
                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211;
                                                                                                                                       Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125.5; DB 1; Length
Pred. No. 0.0041;
6; Mismatches 25; Indels
                                                                                                                                                                                                       29; Indels
                                                                                                                                          DB 1;
                                                                                                                                    34.7%; Score 127; DB 1;
45.2%; Pred. No. 0.0033;
iive 5; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Historne Hi-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M20314; AAA30052.1; -.
PIR; A28100, A28100.
HSSP; P02259; 1HST.
INTERPRO; IPR001386; Histone H1/H5.
INTERPRO; IPR003216; Linkerhist_N.
Pfan; PF00589; linker histone; 1.
ProDom; P0000373; Linkerhist_N.
SMART; SM09526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 РАККАААКРАККААКРАККААКРА 208
                                                                                                                                                                                                                                                                                                                                                                                            50 EKKEYAAAEAKYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYAAAEAKYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.3%;
                                                                                                                                                                                                       38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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RS6 AEDAE
Q9U761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
RS6_AEDAE
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Gavino V.H., Fallon A.M.;

"Aedes mosquitoes ribosomal protein S6 cDNA.";

submitted databases.

-! FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH

-! FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH

AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 AKKVAKKEAKKEVKKVTEAAKKADAKAAKVEPKKADKKSADSGKKATAGDKK----E 309
                                                                                                                                                                        Aedes albopictus (Forest day mosquito).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera,
Culicoidea, Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKA-AEAKKKAKAEAKKYAKAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                   CLASSES OF MRNA (By similarity).
PTW: Ribosomal protein 56 is the major substrate of protein kinases in eukaryote ribosomes (By similarity).
SIMILARITY: BELONGS TO THE SGE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone H., gonadal.
Parechinus angulosus (Angulate sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Echinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.3%; Score 125.5; DB 1
50.0%; Pred. No. 0.0061;
iive 6; Mismatches 25
                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF154066; AAF04789.1; -.
InterPro; IPR001377; Ribossomal S6E.
Pfam; PF01092; Ribossomal S6e; I.
ProDom; PD003460; Ribosomal S6E; I.
PROSITE; PS00578; RIBOSOMAL S6E; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; Phosphorylation
 156 KP-AAKKAAKKPAAKKPAAKKAA 177
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310 KKVEKKAAPAAKKEA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 38; Conservative
                                                                                                                                               40S ribosomal protein S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AKYKAEAAKAAAKEAA 74
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                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-84.
                                                                                                                                                                                                                                 NCBI_TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7658;
                                                                                                                               15-JUN-2002
                                                                                                     15-JUN-2002
                                                                                                                   15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parechinus
                                                                       RS6 AEDAL
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P02256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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셤
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The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and TT free entire primary structure.";

The entire primary structure.";

Eur. J. Biochem. 104:567-578 (1980).

-1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLESSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- SINGELLULAR LOCATION: Nuclear.

                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 80-248.
MEDLINE=80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AKAAAKRKAALAKKKAAAAKRKAAAKAKKAKKYKKAAKKAKKPAKKSPKKAKKPAKKSP 204
                                                                                                        "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYA-KAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Gavino V.H., Fallon A.M.;

"Aedes mosquitoes ribosomal protein S6 cDNA.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH

AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSES OF MRNA (By similarity).
-!- PTM: Ribosomal protein S6 is the major substrate of protein kinases in eukaryote ribosomes (By similarity).
-!- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
                    Strickland W.N., Strickland M., de Groot P.C., von Holt C., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Indels
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1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 123; DB 1;
Pred. No. 0.0071;
9; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA
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                                                                                                                                                                                                                             cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
MEDLINE=80156831; PubMed=6767609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 144 K
248 AA; 26387 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 48.7
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AKYKAEAAKAAAKEAA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way madified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Volckaert G., Yoet M., Robben J.,
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus recorned 15 complete open reading frames, including 2001, BGL2 and BIO2 genes and an ABC tränsporter gene.";
Yeast 13:551-259(1997).
-!- FUNCTION: Z-DNA BINDING PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                   6 KKEKAYAKKAEKAAKK-AEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAA-----A 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUO1 OR YGR285C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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6
                                                                                                                                                                                                                                                                                            33.6%; Score 123; DB 1; Length 346; 45.5%; Pred. No. 0.0092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang S., Lockshin C., Herbert A., Winter E., Rich A.; "Zuotin, a putative Z-DNA binding protein in Saccharomyces
                                                                                                                                                                                                                                                                                                                                25; Indels
                                                                                                                                                                                                 ProDom; PD003460; Ribosomal_S6E; 1.
PROSITE; PS00578; RIBOSOMAL_S6E; 1.
Ribosomal protein; Phosphorylation.
SEQUENCE 346 AA; 39365 MW; S9CFF7B22BDBDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA
                                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-10
                                                                                                                                             EMBL, AF154067; AAF04790.1; -. InterPro, IPR001377; Ribosomal S6E. Pfam; PF01092; Ribosomal S6e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=20B-12;
MEDLINE=93010971; PubMed=1396572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / FY1679;
MEDLINE=97245295; PubMed=9090054;
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306 EKKVEKKAAPAVAKKEA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerevisiae.";
EMBO J. 11:3787-3796(1992)
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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P32527;
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ZUO1_YEAST
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                                                                                                                                                                                             170 J-DÓMAIN.
357 ALA/LYS-RICH.
49019 MW; 0AA76BC11D3C7DAB CRC64;
                                                                                                                                                                                                                                                                    33.6%; Score 123; DB 1; Le
46.2%; Pred. No. 0.011;
tive 10; Mismatches 28;
                                               HSSP, P08622; 1BQZ.
SGD; 50003317; ZUO1.
Interpro; IPR001623; DnaJ.N.
PFam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00036; DNAJ 1; 1.
PROSITE; PS00076; DNAJ 2; 1.
Chaperone; DNA-binding; Nuclear protein.
DOMAIN 306 357 ALA/LYS-RICH.
 : :
                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : :|||| | 350 AKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                      58 EAKYKAEAAKAAAKEAAY 75
EMBL; X63612; CAA45156.1;
                  CAA97317.1;
                                                                                                                                                                                                                                                                                       Best Local Similarity 46.2
Matches 36; Conservative
EMBL; Z73070; CAA9731;
PIR; S25194; S25194.
HSSP; P08622; 1577
                                                                                                                                                                                                                                      433 AA;
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Search completed: March 10, 2003, 12:17:10 Job time: 18.5443 secs

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March 10, 2003, 12:15:01; Search time 40.7743 Seconds (without alignments) 389.109 Million cell updates/sec
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                                                                                                                                                                                                                                                                             671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_bacteria:*
sp_fungl:*
sp_fungl:*
sp_human:*
sp_nammal:*
sp_mammal:*
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sp_phage:*
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Maximum DB seq length: 200000000
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366
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Perfect score:
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                                                      OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			046142 mytilus edu	O46141 mytilus edu	O46143 mytilus edu		O18319 chironomus	O01395 drosophila	Q9ndi9 plasmodium	Q39598 chlamydomon	O65795 triticum ae	Q9h9f1 homo sapien	Q8t5c9 plasmodium	090zd7 bufo bufo g	Q9xh19 triticum ae		Q8t9r3 leishmania		Q23784 chironomus	Q8rxd0 arabidopsis	Q9su08 arabidopsis	Q26907 trypanosoma	Q9h8h4 homo sapien	Q98wu2 triticum ae	Q9ru45 deinococcus	Q9v6s7 drosophila	Q9y1p8 plasmodium	Q9swu3 triticum ae
	16 Q8Y5W4	10 065794	5 046142	5 046141	5 046143	_	5 018319	_	o			4 Q9H9F1	-	13 Q90ZD7	10 Q9XHL9			5 046140	α	10 Q8RXD0	10 Q9SU08	5 Q26907	4 Q9H8H4	10 Q9SWU2	16 Q9RU45	5 Q9V6S7	5 Q9Y1P8	10 Q9SWU3
755	239	284	191	191	191	191	233	275	696	265	288	467	1671	224	275	98	111	191	243	485	924	68	198	237	581	607	845	236
33.3	33.2	32.9	32.7	32.4	32.4	32.4	32.4	32.4	32.2	32.1	32.1	32.0	31.8	31.7	31.7	31.6	31.6	31.6	31.6	31.6	31.6	31.1	31.1	31.1	31.1	31.1	31.0	30.9
122	121.5	120.5	119.5	118.5	118.5	118.5	118.5	118.5	118	117.5	117.5	117	116.5	116	116	115.5	115.5	115.5	115.5	115.5	115.5	114	114	114	114	114	113.5	113
17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	. 40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

	65 PRELIMINARY; PRT; 394 AA.	00 [ addition / 0000	(Tremburel. 20,	(TrEMBLrel. 20, Last		Membrane spanning protein, required for outer membrane integrity		OR 20907 OR ECS0774.	Escherichia coli O157:H7.	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		NCBI_TaxID=83334;		SEQUENCE FROM N.A.	IN=O157:H7 / EDL933 / ATCC 700927;	MEDLINE=21074935; PubMed=11206551;	Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,	Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,	beck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,	aca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,	Welch R.A., Blattner F.R.;	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";	Nature 409:529-533 (2001).		SEQUENCE FROM N.A.	STRAIN=0157:H7 / RIMD 0509952;	INE=21156231; PubMed=11258796;	shi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,	Han CG., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,	lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,	Kuhara S., Shiba T., Hattori M., Shinagawa H.;	"Complete genome sequence of enterohemorrhagic Escherichia coli	0157:H7 and genomic comparison with a laboratory strain K-12.";	DNA Res. 8:11-22(2001).	; AE005252; AAG55075.1;	EMBL; AP002553; BAB34197.1;
965	Q8X965	Q8X965;	OI-MAK	01-MAR	01-5UN	Membra	(Membr	TOLA O	Escher	Bacter	Escher	NCBI_T	ا Ξ	SEQUEN	STRAIN	MEDLIN	Perna	Rose D	Posfai	Grotbe	Apodac	Welch	"Genom	Nature	[2]	SEQUEN	STRAIN	MEDITIN	Hayash	Han C.	Iida T	Kuhara	"Comp]	O157:H	DNA Re	EMBL;	EMBL;
08X965	Ω	A R	5	텀	F	DE	DE	Ŋ	SO	ပ္ပ	ဗ	ŏ	RN	RP	RC	ž	æ	æ	RA	RA	æ	Ą	RT	RL	N.	RP	RC	ΚX	RA	R.	Æ	Ą	RT	КŢ	RL	R G	ž

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MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                  SEQUENCE FROM N.A.
             NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tola protein.
  Salmonella
                                                                                                                                                                                                                                                                            Query Match
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Q937K4
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                                                                                Gaps
                                                                                                                   138 AAKAAADAKAKAEADDKAAEEAAKKAAADDAKKKAEAEAAKAAAEAQKKAEAAAAALKKKA 197
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21534948; PubMed=11677609; MCCIlelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., MCCOurtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., Gomplete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AKKKABABA--AKAAABAKKKABABAAKAAABAKKKADABAK--AAABAKKKADAAAK 244
                                                                                                       1 AKKYAKKEKAYA----KKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA-----KA 49
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                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
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                                                          Length 394;
                                                                                21; Indels
                                   5B58D8E8230BDE28 CRC64;
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Last annotation update)
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                                                         Score 148; DB 16;
Pred. No. 0.00017;
                                                40.4%; Scor.
55.1%; Pred. No. o...
7; Mismatches
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TOLA OR STM0747.
Salmonella typhimurium.
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                                                                                                                                                               55 AAAEAKYKAEAA-----KAAAKEAA 74
                                                                                                                                                  50 EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=LT2 / SGSC1412 / ATCC 700720;
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InterPro; IPR000104; Antifreeze_1. PRINTS; PR00308; ANTIFREEZEI.
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InterPro; IPR000104; Antifreeze I.
PRINTS; PR00308; ANTIFREEZEI.
                                  394 AA; 40517 MW;
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                                                Query Match
Best Local Similarity 55.1%
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1es 49; Conservative
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE 407 AA:
                        Complete proteome
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STY0793.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bascham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servora Typhi (T18.";
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Pectobacterium.
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Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
"characterization of the Erwinia chrysanthemi tol-pal genes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAC82708.1; -. SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
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Last annotation update)
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54.4%; Pred. No. 0.00023;
tive 7; Mismatches 14;
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                                                                                                                                                                                                                                                                          Nature 413:848-852(2001).
EMBL; AL627268; CAD05209.1; -.
Interpro; IPR00104; Antifreeze.1.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q937K4;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity
Matches 41; Conserv
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SEQUENCE
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Q39576
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061164
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                                                                                                                                                                                                                                                                                                                                                                Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
"Lacteriol. 1785836-5840(1996).
EMBL; X74218; CAB50780.1;
InterPro; IPR001386; Histone—H1/H5.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J., "The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                          STRAIN=MT-2;
Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                          Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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46.9%; Pred. No. 0.00043;
iive 10; Mismatches 21
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            372
                                 Created)
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                                                                                                                                                                                              ceîl`envelope.";
J. Bacteriol. 178:1699-1706(1996).
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MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                     MEDLINE=96198174; PubMed=8626299;
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                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20, TolA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Conservative
          PRELIMINARY;
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                                                                                                                                                                                                                                                 Ramos-Gonzalez I.;
Submitted (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                 Pseudomonas putida
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                    FROM N.A.
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                                                                                                    Pseudomonas.
NCBI_TaxID=303;
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SEQUENCE
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           Q9WWX1
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Q9CM70
09WWX1
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SEQUENCE FROM N.A.
MEDLINE=56120662; PubMed=8590479;
Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R. Fabry S., Muller K., Lindauer A., Fark P.B., Cornelius T., Schmitt R. Fabry S., Muller K., Lindauer and regulatory elements of Chlamydomonas histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
EMBL; U16726; AA89452.1;
HSSP; P02259; 1HST.
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                                                                                                                                                                                                                                                                                                                                                                         14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYA-----KKEKAYAKKAEKAAKKAE-AKAYKAAEA---KKKAKAEAKKYAKAAKAE- 50
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AR006136; AAXO3052.1; -.
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Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                            Query Match 38.3%; Score 140; DB 16; Length 389; Sest Local Similarity 50.5%; Pred. No. 0.0007; Aatches 46; Conservative 10; Mismatches 21; Indels 14
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                                                                                                                                                                                                                                                  389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
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Last sequence update)
Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 15, Last annotation update)
Brythrocyte binding protein.
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49.4%; Pred. No. 0.00061;
ative 4; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; 1.
                                                                                                                      HSSP; P19934; ITOL.
InterPro; IPR000533; Tropomyosin.
PRNINTS; PR00194; TROPOMYOSIN.
Complete proteome.
SEQUENCE 389 AA; 42197 MW; B41
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"Interruption of a Trypanosoma cruzi gene encoding a protein containing 14-amino acid repeats by targeted insertion of the neomycin phosphotransferase gene.";
Mol. Biochem. Parasitol. 57:317-330(1993).

EMBL: L04603; AAA96494.1;
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                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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InterPro; IPR001230; Prenyl site.
PROSITE; PS00294; PRENYLATIÖN; UNKNOWN 1.
SEQUENCE 1128 AA; 119686 MW; 7997745D32B83656 CRC64;
                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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STRAIN=SYLVIO X-10;
MEDLINE=93165082; PubMed=8381919;
Otsu K., Donelson J.E., Kirchhoff L.V.;
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SEQUENCE 388 AA;
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                                                                                                                                     R27-2 protein.
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Q8ZGZ2;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAA-KAEKKEYA--- 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                               Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
"A family of chimeric erythrocyte binding proteins of malaria parasites.";
parasites.";
EMBL, Acad. Sci. U.S.A. 95:1230-1235(1998).
EMBL, AF031886; AAC05366.1; -.
SEQUENCE 1701 AA; 199268 WW; EDA8E2DEFD87CE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%; Score 138; DB 5; Length 1701; 54.4%; Pred. No. 0.0043; Live 8; Mismatches 16; Indels 1;
                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EMBL, AP002997; BAB48847.1, -.
Hypoth Atical Protein; Complete proteome.
SEQUENCE 1341 AA, 138670 MW, 79CSD8149C969BC8 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll1482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti)
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MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                   MEDLINE=98115903; PubMed=9448314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Conservative
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Matches 43; Conservative
                                   Plasmodium yoelii yoelii
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                                                                                              NCBI_TaxID=73239;
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Length 1128;

23; Indels

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MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
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                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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388 AA
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TOLA OR YPO1123.
PRT;
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InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
PRELIMINARY;
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EMBL; AJ006637; CAA07165.1; -.
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01-JUN-2002 (
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SEQUENCE
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Q84528;
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Q84528
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Gaps
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Kaiser B., Kunkel W., Saluz H.P., Munder T.,

"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKA--KAEAKKYAKAAKAE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans (Yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.0%; Score 128; DB 16; Length 200; 50.0%; Pred. No. 0.0032; ive 3; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Probable histone H1 protein.
RSC2793 OR RS00453.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 43; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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214 VEVAEKAAADAA 225
                                                                                                 63 AEAAKAAAKEAA 74
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1274 AKKAEEARKAEBAAKKAEAARKAEBAAKKAEEARKAEEARKAEBARKAEBARKAEA 1333
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MEDLINE=96187795; PubMed=8614977;
Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map positions 88 to 182.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs in
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                                                     34.3%; Score 125.5; DB 3; Length 212; 47.9%; Pred. No. 0.0054; Live 9; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium vivax.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 0:0-0(2012).
EMBL, AY042083; AAL105508.11.-
SEQUENCE 1866 AA; 212420 WW; DC692D7CFAE7D93F CRC64;
212 AA; 24231 MW; 10C2122E9554A387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 34.0%; Score 124.5; DB 5; Local Similarity 50.0%; Pred. No. 0.054; Pred 42; Conservative 10; Mismatches 23;
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(TrEMBLrel. 21, I
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                                                                           Local Similarity 47.9
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SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
MEDLINE=20013326; PubMed=10544099; States A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Ven Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.5%; Score 122.5; DB 12; Length 311; 48.6%; Pred. No. 0.013; tive 9; Mismatches 26; Indels 3;
                                                                                                                                                                                                                                                                    [5]
SEQUENCE FROM N.A.
Van Etten J.L.;
Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        SECURINCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U42580; AAC96576.1; -.
InterPro; IPR002048; BF-hand.
PROSITE; PS000189; BF-hand.
SEQUENCE 311 AA; 35390 MW; 9780E9582AFEF88A CRC64;
                                                                                                                                                                                                                                       Van Etten J.L.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                             Virology 263:254-262(1999)
                                                                                                                                                                                        Virology 276:27-36(2000)
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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1 AKKYAKKEKAYAKK-AEKAAKKAEAKAYKAAEAK--KKAKAEAKKYAKAAKAEKKEYAAA 57
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Best Local Similarity 48.6 Matches 36; Conservative

Local Similarity

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Gaps

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58 EAKYKAEAAKAAAK 71

126 EKAPAREAAKAAK 139

Search completed: March 10, 2003, 12:25:57 Job time: 41.7743 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

March 10, 2003, 12:15:01 ; Search time 40.1245 Seconds (without alignments) 255.712 Million cell updates/sec

US-09-816-989A-5

Perfect score:

Sequence:

**BLOSUM62** Scoring table:

908470 seqs, 133250620 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDS2/gcgdata/geneseq/geneseqp Database

| SIDS2/gcgdata/geneseq/geneseqp.embl/AA1990.DAT:\*
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'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT /SIDS2/gcgdata/geneseg /gcgdata/geneseg/ /SIDS2/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Copolymer molecula	Peptide #10 used i	Amino acid polymer	Poly-Lys-Ala used	Nucleic acid trans	Recombinant copoly				
ΩI	AAY82575	AAY82576	AAY82577	AAY82574	AAY82573	AAY98499	AAY59044	AAU04289	AAB45852	AAR06445
	21	21	21	21	21	21	21	22	22	11
% Query Match Length DB	77	98	109	99	26	100	100	100	100	154
% Ouery Match	100.0	96.0	79.0	77.2	67.1	39.5	39.5	39.5	39.5	38.9
Score	366	351.5	289	282.5	245.5	144.5	144.5	144.5	144.5	142.5
Result No.	-1	7	е	4	w	9	7	80	6	10

Recombinant copoly Trypanosoma cruzi	Copolymer molecula	Mycobacterium bovi	Trypanosoma cruzi	Trypanosoma cruzi	M. tuberculosis hi	M. tuberculosis hi	Zuotin. Saccharom	Human zuotin prote	S cerevisiae apopt	Synthetic helical	Listeria monocytog	Amino acid sequenc	Human DNA modifica	Human protein sequ	C albicans apoptos	Quail H1 histone p	Human protein sequ	Drosophila melanog	Plasmodium yoelii	Human protein sequ		Human histone H1 i	Human histone H1 i	Histone H1 isoform	Human histone H1.5	Human histone H1 i	Human histone H1 i	Novel human diagno	Peptide fragment o	Human linker histo	T. cruzi L19E homo	TcE protein sequen	TCE antigen of Trp
. AAR06446 5 AAR84568				5 AAR84565	) AAY34055		3 AAW30256	) AAY32954		1 AAR25206			: AAU03592	: AAB94309			2 AAB95499		·	2 AAM25508	1 AAW29476				•		. AAY57358	: ABG28693	AAU09945	AAE13237	/ AAW06913		AAY23306
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11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

AAY82575 standard; peptide; 77 AA. AAY82575

AAY82575;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5. 

glatiramer accate, autoimmune disease, antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antibaoriatic; dermatory; antidabetic; thyromimetic; haemostatic; antibaoriatic; dermatological; antianaemic; immunosuppressive; demyolinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US22402. 24-SEP-1999; 98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

98US-0101693.

24-SEP-1999; 25-SEP-1998;

06-APR-2000.

(YEDA ) YEDA RES & DEV (TEVA-) TEVA PHARM USA

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glather actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or mutibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune haemolytic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gillain-Barre's syndrome, Hashimoco's disease, dilapathic myxoedema, myasthenia gravis, psyndrome, Hashimoco's disease, idiopathic myxoedema, myasthenia gravis, psyndrome, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft isease, graft-versus-se, and delayed-type hypersenaitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to molecular accate molecules, which makes them ideal for use as
                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English
                                                                                   WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AA;
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ö Gaps 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYYAKAAKAEKKEYAAAEAK 60 ; 0 100.0%; Score 366; DB 21; Length 77; 100.0%; Pred. No. 3.2e-27; cive 0; Mismatches 0; Indels Local Similarity 100. nes 77; Conservative Matches 셤 ઠે

61 YKAEAAKAAAKEAAYEA 77 ઠે

61 YKAEAAKAAAKEAAYEA 77

AAY82576 standard; peptide; 86 AA. AAY82576; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

(first entry)

28-JUL-2000

Copolymer; molecular weight marker; TV-marker; immune disease; glatiframer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; condition; multiple sclerosis; rheumatoid arthritis; condition; multiple sclerosis; rheumatoid arthritis; choin's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

28-JUL-2000 (first entry)

AAY82577;

Copolymer; molecular weight marker; TV-marker; immune disease;

. WO200018794-A1.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple concertaintis, autoimmune thyroiditis, autoimmune haemolytic anaemia, autoimmune cophoritis, outcoimmune thrombocytopaenia uveoretinitis, crohn's disease, chronic immune thrombocytopaenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves (Dupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-staft diseases, gasembicus, psoriasis, psoriasis, pemphigus vulgaris, or systemic include host-versus-staft disease, gasethy disease, and delianed molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                            molecular weight markers for prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Length 86;
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89.5%; Pred. No. 8.1e-26;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                            Copolymer 1 related polypeptides used as glatiramer acetate and for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY82577 standard; peptide; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YKAEAAKAAAKEAAYEA 77
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                                                                                                                                                                                                                                                                                                                    Claim 10; Page 14; 72pp; English.
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les 77; Conservative
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us-09-816-989a-5.open.rag

glatitamer actate; autojamum disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

28-JUL-2000 (first entry)

Copolymer; molecular weight marker; TV-marker; immune disease;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune attibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, theumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinits, crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves diseases, Gullain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psemphigus vulgaris, or systemic lund, a betreated mediated mediated diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the cancact sen
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                            Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
      inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                             pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                       99WO-US22402
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                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1999;
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                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                 06-APR-2000.
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(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Lis D;

Gad A,

99WO-US22402.

24-SEP-1999; 25-SEP-1998;

36-APR-2000.

WO200018794-A1

Jnidentified

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple scleonis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic uveoretinitis, Crohn's disease, fundic immune thyroiditis, autoimmune uveoretinitis, crohn's disease, chonic immune thyroiditis, autoimmune purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
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84.4%; Pred. No. 1.5e-19;
ive 0; Mismatches 1
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Best Local Similarity 84.49
Marches 65, Conservative
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셤
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Pred. No. 6.5e-20;
1; Mismatches 3; Indels 33
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1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA-

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Query Match 79.0%; Best Local Similarity 67.0%; Matches 73; Conservative 1

AAY82574 standard; peptide; 66 AA

AAY82574;

AAY82574 ID AAY8 XX AC AAY8 XX

RESULT 4

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4,

50 YKAEAAKAAAKEAAYEA 66

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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabbetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                 AAY82573 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English.
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                                  AAY 82573
AAY 82573
AAY 82573
AAY 82573
AAY 82573
AAY 82573
AAY 8273
AAY 82
RESULT 5
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antibody-mediated diseases uch diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune purpura, contaits, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dilabetes mellitus, Graves disease, dilabetes mellitus, Graves disease, dilabetes mellitus, Graves include host-versus-graft gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypoptides of the invention have defined molecular weights and physical properties which are analogous to glatirame acctate molecules, which makes them ideal for use as AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acceate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases thich may be treated include either cell-mediated or site. molecular weight markers

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67.1%; Score 245.5; DB 21; Length 56;
56 AA
Sequence
                          Query Match
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Gaps

<u>ب</u>

Indels

DB 21; Length 100;

Score 144.5; DB 21; Pred. No. 1.5e-06; 6; Mismatches 23;

39.5%;

100 AA;

Sequence Query Match Best Local

al Similarity 58.4%; 45; Conservative

Matches

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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The sequences AAA3633-A3652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver concleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgonic animals (as models or human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in include transforming cells to produce proteins or transfecting cells in the include the cellular capacity of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent-linked to nucleic acid, surface ligand and lytic agent
                   21; Gaps
                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAKAKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                           Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
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                   Indels
                                                                                                                                                                                                                                                                                                                                                                          Peptide #10 used in nucleic acid transporter system.
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72.7%; Pred. No. 3.5e-16;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                            AAY98499 standard; Peptide; 100 AA.
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                                                                                                                                                    40 YKAEAAKAAAKEAAYEA 56
                                                                                                                             61 YKAEAAKAAAKEAAYEA 77
                   56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-281993/24.
 Best Local Similarity
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                     Matches
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DB 21; Length 100;

셤 8

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23
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                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
3..100
/note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                 pport system; NTS; cell surface receptor; cytosis;
lysis moiety; transgenic animal; human disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                      Amino acid polymer seq ID NO: 64 of US5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                     AAY59044 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                       nuclear membrane; İysis moiety
nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0460890,
                                                                                                                                                                                                                                                      (first entry)
                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cristiano RJ,
                                                                 AKYKAEA-AKAAKEAA
                                                                                                                                                                                                                                                                                                                       transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-038262/03.
                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Misc-difference
                                                                                                                                                                                                                                                                                                                       Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                      07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5994109-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                     AAY59044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOO SLC,
                                                                                                                                                    RESULT 7
                                                                                                                                                                     AAY59044
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100 AA;

Sequence

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3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules is used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                      Gaps
                                                                                                    1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference 3..100 may be present
/note= "Lys-Ala in positions 3-100 may be present
absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                   3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-Lys-Ala used in nucleic acid transporter system.
39.5%; Score 144.5; DB 21;
llarity 58.4%; Pred. No. 1.5e-06;
Conservative 6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 131; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              AAU04289 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith LC, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0167641.
92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                  АКАКАКАКАКАКАКА 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
.....hes 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-365933/38
  Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
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AAR06445 standard; protein; 154 AA.

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RESULT 10
                                                                                          AAR06445
                셤
                                                                                                             This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The mucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can carbo be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor appressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                         Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor autigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                         Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                             AAB45852 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0460971
                                                                                                                                                                                                                                     (first entry)
                                   AKYKAEA-AKAAAKEAA 74
                                                                     AKAKAKAKAKAKAKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1993;
20-MAR-1992;
                                                                                                                                                                                                                                     21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1993;
                                                                                                                                                                                                 AAB45852;
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                                                                     62
                                   59
                                                                                                                                            AAB45852
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 2-NOV-1984 US4691009, NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. Cequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, ARK, AKK, and AAA. The N-terminal alamine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune control a checkhalowyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 KKYKKBAEEBEYKKKAKEAERAKKAKYKKKKGAEAAKAAKAAAAAAYKKEAEAAAEAEK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 154;
                                                                                                                                                                    copolymer 1; COP-1-77; myelin basic protein; MBP; l activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing genes encoding random polymers of aminoacid(s) - 1 producing recombinant polypeptide(s) with biological and/or
                                                                                                           Recombinant copolymer 1-77, myelin basic protéin analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KKYAKAAKAEKKEYAAABAKYKABAAKA-----AAKEAAYE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 142.5; DB 1
43.4%; Pred. No. 3.7e-06;
iive 10; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0473845.
89US-0312541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            90EP-0301700.
                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-255848/34.
                                                                                                                                                                                                                               multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also AAQ05665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ05664.
                                                                                                                                                                                                 immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1989;
                                                        03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1990.
                                                                                                                                                                                                                                                                                                                                              EP383620-A.
                                                                                                                                                                                                                                                                                        Synthetic.
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AAR06445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cook KS;
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58 

59 AKYKAEA-AKAAAKEAA 74

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6; Mismatches

Conservative

45;

Matches

Local Similarity

Query Match

39.5%; Score 144.5; DB 22; Length 100; 58.4%; Pred. No. 1.5e-06;

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80 KKAEKAKAAEKAKAAYK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTSU K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kirchhoff LV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                      WO9525797-A1
                                                                                                                                                 09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1995.
                                                                                                                  AAR84568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OTSU/)
                                                                                                                                                                                                                                                                                                    Key
Region
                                                  RESULT 12
                                                                   AAR8456
                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding for CCD-1-19 were subcloned from PREV 2.1 to pBG3-26eltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleocide duplexes incoding the following segments: YKK, AAE, KAK, KKA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control ademyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 38.3%; Score 140; DB 11; Length 106; 1 Similarity 54.5%; Pred. No. 4.2e-06; 42; Conservative 7; Mismatches 22; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                                                                                  Recombinant copolymer 1-19, myelin basic protein analogue.
72 AKYKKKAKEAEYKKKAKAAABEAEYKKEAEEAEYKKYKKKAKKAKYK 117
                                                                               AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0473845.
89US-0312541.
                                                                                                                                                                                                                                                                                                                                                                                    90EP-0301700
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-255848/34.
N-PSDB; AAQ06446.
                                                                                                                                                                                                                                   immunological activ:
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1990;
                                                                                                                                                 03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1990;
17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                  22-AUG-1990.
                                                                                                                                                                                                                                                                                                                  EP383620-A.
                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                AAR06446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-5-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and allow the company of a highly conserved 14 as sequence and a 68 as C-terminal region. This sequence encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69
(CC repeat units and also contains the amino and carboxy terminal
(CC the diagnosis of Chagas disease (American Trypanosomiasis), they are capable of detecting anti-T.cruzi antibodies; or for blood screening. The TCR27 protein has epitopes to which most T.cruzi
(CC are capable of detecting anti-T.cruzi antibodies; or for blood screening. The TCR27 protein has epitopes to which most T.cruzi
(Infected individuals have antibodies. The TCR27 polypeptides will not react with serum from patients with leishmaniasis, schistosomiasis,
(CC react with serum from patients with leishmaniasis, schistosomiasis,
(CC automimmune disease and are hence less likely to cause false
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a
immunoassay reagent for specific diagnosis of Chagas disease, also
related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= repeat region /note= "16 of \overline{6}9 repeat units of 14 amino acids"
                                                                                                                                                                                                                                                                                                                                         TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
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                                                                                                                                                                                                                                                         Trypanosoma cruzi TCR27 polypeptide, Ag15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
AAR84568 standard; Protein; 643 AA.
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                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KIRC/) KIRCHHOFF L V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-344618/44.
N-PSDB; AAT05332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma cruzi.
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61 YKAEAAKAAAK-EAAYE 76

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32; Gaps

Indels

Pred. No. 1.1e-05;

50.68;

39; Conservative

Matches

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Best Local Similarity

0; Mismatches

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAFAKKYAKAAKAEKKEYAAAEAK 60

1 AKKYAKK----AKAEKA-----KKAYKAAEAKKAAKYE----

45

30 -KAAAEKAAKEAAYEA

61 YKAEAAKAAAKEAAYEA 77

547 TKVAEAEKQKAAEAA 561

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glaticamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or altoimmune CC antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple collerosis, rheumatoid arthritis, osteoarthritis autoimmune hamolytic ansemia, autoimmune opphoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thyroiditis, untoimmune cophoritis, autoimmune thrombocytopaenia purpura, collitis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimoto's disease, aliopathic myxoedema, myasthenia gravis, psyndrome, Hashimoto's disease, and delated-molecular weights and physical properties of the invention have defined molecular weights and physical properties of the invention have constrained acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myashhenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                              Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                         AAY82572 standard; peptide; 45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US22402.
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USA INC.
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 AA
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                                                                                                                                  28-JUL-2000
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                                                                                 AAY82572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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RESULT 13
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35.8%; Score 131; DB 21; Length 45;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAVKATKSPAKKVTKAVKKTAV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used faignosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                       Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKAEKAAKKA--EAKAYKAA-----EAKKKAKAEAKKYAKAAKAEKK 52
                                                                                                                                        MDP1; slow growing acid-fast bacterium protein; immunogenicity; pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC; Mycobacterium avium intracellular complex; Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.5%; Score 130; DB 21; Length 205; 49.4%; Pred. No. 7.2e-05; ive 7; Mismatches 26; Indels 10
                                                                                           Mycobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
AAB20575 standard; Protein; 205 AA.
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KASVRKAATKAPAKKAAAKRPATKA 193
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                                                                                                                                                                                                                                                                                                28-JAN-2000; 2000WO-JP00455
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                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as tuberculosis
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                                                                                                                                                                                                      Mycobacterium bovis
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                                                              08-DEC-2000
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                                AAB20575;
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(MATS/)
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ARR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi

The proteins are all fusion products with glutathione-5-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises

C a 95 amino acid (aa) N-terminal region; 69 repeats of a highly
C conserved 14 as sequence and a 68 as C-terminal region. This sequence
c encodes the GST sequence and a 68 as C-terminal region. This sequence
repeat units and also contains a linker sequence. The TCR27
polypeptides of the invention are useful for the diagnosis of Chagas
disease (American Trypanosomiasis), they are capable of detecting
anti-T.cruzi antibodies; or for blood screening. The TCR27 protein
c antibodies The TCR27 polypeptides will not react with serum from
c antibodies. The TCR27 polypeptides will not react with serum from
C patients with leishmaniasis, schistcosomiasis, or autoimmune disease
and are hence less likely to cause false positives in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a
immunoassay reagent for specific diagnosis of Chagas disease, also
related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
241..450
/label= repeat_region
/note= "15 of 69 repeat units of 14 amino acids"
                                                                                                                                                                                                                                                                                                                                                        TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
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35.5%; Score 130; DB 16; Length 472;
Best Local Similarity 51.4%; Pred. No. 0.00018;
Matches 38; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                     Trypanosoma cruzi TCR27 polypeptide, Ag8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 44-45; 68pp; English
                                                                   AAR84569 standard; Protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US03191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0216894
                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirchhoff LV, Otsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-344618/44.
N-PSDB; AAT05333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1995;
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                                                                                                                                      AAR84569;
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Region
RESULT 15
                          AAR84569
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Gaps

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360 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 416

417 TKVÁÉÁEKOKÁAÉÁ 430

60 KYKAEAAKAAKEA 73

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59

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Search completed: March 10, 2003, 12:21:30 Job time : 41.1245 secs
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein March 10, 2003, 12:26:10 ; Search time 22.9051 Seconds (without alignments) 141.764 Million cell updates/sec Run on:

US-09-816-989A-5 366 Title: Perfect score:

1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 77 Sequence:

**BLOSUM62** 

Scoring table:

Gapop 10.0 , Gapext 0.5

188354 seqs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| Cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*
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| Cgn2\_6/ptodata/1/pubpaa/USO6\_PUBGOMB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ID Description	US-09-816-989A-5 Sequence 5,					US-09-820-843A-8 Sequence 8, Appli	2 Sequence 2	US-10-184-832-5 Sequence 5, Appli	01 Sequence 20	US-09-820-843A-27 Seguence 27,	US-09-816-989A-1 Sequence 1, Appli	US-09-820-843A-24 Sequence 24, Appl	US-09-864-761-36182 Sequence 36182,	US-09-820-843A-95 Sequence 95, Appl		Sednence 30	Sequence 90,	Sequence 90, Sequence 48,	Sequence 90, Sequence 48, Sequence 3,	Sequence 90, Sequence 48, Sequence 3, Sequence 13
	DB	101	10	10	10	2	σ	10	σ	თ	σ	10	σ	10	σ	σ	٠	0	י ס	6 6	622
	Query Match Length DB	77	86	109	99	56	372	45	452	223	326	35	309	617	369	102		010	218	218	218 434 892
dю	Query Match	100.0	96.0	79.0	77.2	67.1	38.5	35.8	34.0	33.1	30.5	28.6	28.6	28.6	27.9	27.0		27.0	27.0	27.0	27.0 27.0 26.9
	Score	366	351.5	289	282.5	245.5	141	131	124.5	121	111.5	104.5	104.5	104.5	102	66		0	66	6 6 6 6	9 9 9 9 9 9 9 9
	Result No.	1	7	٣	4	S	9	7	œ	σı	10	11	12	13	14	15		16	16	16 17	16 17 18

Sequence 5197, Ap Sequence 5298, Ap Sequence 12094, A Sequence 100, App Sequence 23, Appl Sequence 21, Appl Sequence 37061, A Sequence 11216, A Sequence 164, Ap Sequence 18, Appl Sequence 1, Appli Sequence 5, Appli Sequence 1, Appli Sequence 265, Appli 265, Ap	Sequence 10575, Ap Sequence 4893, Ap Sequence 35241, A Sequence 7, Appli Sequence 2, Appli Sequence 259, App
US-09-738-626-5197 US-09-815-242-5298 US-09-915-242-12294 US-09-919-497-100 US-09-919-724-46 US-09-919-724-46 US-09-919-724-46 US-09-815-243-1216 US-09-815-243-1216 US-09-815-243-1216 US-09-815-242-5198 US-09-815-242-5198 US-09-815-242-5198 US-09-915-318-1105-093-893-580-8 US-09-913-508-893-580-8 US-09-913-580-8 US-09-913-813-1105-093-893-238-11	US-09-815-242-10575 US-09-815-242-4893 US-09-864-761-35241 US-09-923-304-2 US-09-925-302-559
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93 99 99 99 99 99 99 99 99 99 99 99 99 9	877 877 86 85.5 85.5
01000000000000000000000000000000000000	1 4 4 4 4 10 11 12 12 14 15

# ALIGNMENTS

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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: CODOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1999-09-24
SOFTWARE: 1999-09-24
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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100.0%; Score 366; DB 10; Length 77;
Best Local Similarity 100.0%; Pred. No. 6e-26;
Matches 77; Conservative 0; Mismatches 0; Indels
Sequence 5, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKYAKAEAKKEYAAAEAK 60 YKAEAAKAAAKEAAYEA 77 YKAEAAKAAAKEAAYEA 77 61 61 8 g 셤

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RESULT 2 US-09-816-989A-6 ; Sequence 6, Application US/09816989A

US20020115103A1

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APPLICANT: Lis, Dorien TREADENTED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKET TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKET TITLE OF INVENTION: AND FOR THERABEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR PALICATION DATE: 1998-09-25 PRIOR APPLICATION NUMBER: PCT/US99/22402 PRIOR PRING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lis, Doris
TITLE OF INVENTUAL COOCLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKHITLE OF INVENTUAL COPOLYMER 1 USE OF USE
FILLE REPERENCE: 2609/60807-A-PCT-US
FILLE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 2609/6916, 989A
FILME APPLICATION NUMBER: 60/101, 693
FRIOR APPLICATION NUMBER: 60/101, 693
FRIOR PAPLICATION NUMBER: PCT/US99/22402
FRIOR PAPLICATION DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.2%; Score 282.5; DB 10; Length 66; Best Local Similarity 84.4%; Pred. No. 9.6e-19; Matches 65; Conservative 0; Mismatches 1; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 56;
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                                                                       Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFWARE: Patentin version 3.1
SEQ ID NO LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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SEQ ID NO 3
LENGTH: 56
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Best Local Similarity
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US-09-816-989A-3
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Facent No. US2002015103A1

GENERAL INFORMATION:
APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

PRIOR APPLICATION NUMBER: US/09/816,989A

PRIOR PLIING DATE: 1998-09-25

PRIOR PLIING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATCHIL VERSION 3.1

SEQ ID NO S: 7

LEMAND. 1.00
          APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: WUMBER: US/09/616,989A
CURRENT APPLICATION NUMBER: G0/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.0%; Score 351.5; DB 10;
llarity 89.5%; Pred. No. 1.2e-24;
Conservative 0; Mismatches 0;
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Pred. No. 4.4e-19;
1; Mismatches 3;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.0%;
Matches 73; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
GENERAL INFORMATION:
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Sequence 201, Application US/10051643

Publication No. US20020197265A1

Fubblication No. US20020197265A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008c2

CURRENT APPLICATION NUMBER: US09/156,181

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SEQ ID NO 201

LENGTH: 223
                                                                                                                                                                                                                                                                                    NS-10-184-832-5

1 Sequence 5, Application US/10184832

2 Sequence 5 Application US/10184832

3 Sequence 5. Application No. 220030022857A1

3 GENDRAL INFORMATION:

3 APPLICANT: Xu et al.

4 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

5 TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

5 TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

6 CURRENT APPLICATION NUMBER: 2010-05-62-8

7 TORRENT FILING DATE: 2002-06-28

7 PRIOR APPLICATION NUMBER: 60/303,250

7 PRIOR FILING DATE: 2001-07-05

7 NUMBER OF SEQ ID NOS: 6

7 SOFTWARE: FASELSEQ for Windows Version 4.0

7 SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                               1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE-
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                                                                                                                                                                 61 YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :|:| ||| |||
152 AKAEAKAEAKAEAKE 166
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US-10-184-832-5
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US-10-051-643-201
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                                                                                                                                                                                                     Sequence 8, Application US/09820843A
Sequence 8, Application US/09820843A
Sequence 8, Application WS/03803039963A1
GENERAL INFORMATION:
TITLE OF INVENTION: A COMPUTATIONAL WETHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USFFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT PAPLICATION NUMBER: US/09/820,843A
CURRENT PILION DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 AKRLAAAAKQAEBEAKAKAABIAAQKAKQEAEAKAKLEAEAKAKAVAEAK--AK-AEAEA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.5%; Score 141; DB 9; Length 372; Best Local Similarity 54.7%; Pred. No. 1.2e-05; Matches 47; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc_feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
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Batent No. US20020115103A1

GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
ITILE OF INVENTION: COOLUMER I RELATED POLYPEP':
ITILE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2010-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PT/US99/22402
PRIOR APPLICATION NUMBER: PT/US99/22402
PRIOR PILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 2
LENGTH: 45
1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 KAKAAAEAKAKADAEAKAATEAKRKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 KEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                    40 YKAEAAKAAAKEAAYEA 56
                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.8
Best Local Similarity 50.6
Matches 39; Conservative
                                                        61 YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-816-989A-2
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us-09-816-989a-5.open.rapb

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Sequence 24, Application US/09820843A
Publication No. US20030039953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Council Of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: O63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ## STREAGE NO. US2020148763A1

| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. |
| APPLICANT: Penn, Wensher
| APPLICANT: Penn, Wensher
| APPLICANT: Chen, Wensher
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US 09964,761
| CURRENT APPLICATION NUMBER: US 60/180,312 |
| CURRENT PILING DATE: 2000-02-04 |
| PRIOR APPLICATION NUMBER: US 60/207,456 |
| PRIOR FILING DATE: 2000-03-06 |
| PRIOR PILING DATE: 2000-08-03 |
| PRIOR FILING DATE: 2000-08-03 |
| PRIOR FILING DATE: 2000-09-06 |
| PRIOR FILING DATE: 2000-09-07 |
| PRIOR PILING DATE: 2000-09-07 |
| PRIOR FILING DATE: 2000-09-07 |
| PRIOR PILING DATE: 2000-09-27 |
| PRIOR FILING DATE: 2000-09-27 |
| PRIOR FILING DATE: 2000-09-27 |
| PRIOR FILING DATE: 2001-01-30 |
| PRIOR APPLICATION NUMBER: PCT/US01/00666 |
| PRIOR FILING DATE: 2001-01-30 |
| PRIOR FILING DATE: 2001-01-30 |
| PRIOR FILING DATE: 2001-01-30
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAK--KEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAKAEAKKYAK-AAKAEK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: misc feature
CTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF
NAME/KEY: misc feature
CTHER INFORMATION: gi|9951352
US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.6%; Score 104.5; DB 9; Length Best Local Similarity 48.9%; Pred. No. 0.015; Matches 43; Conservative 0; Mismatches 34; Indels
                                   Indels
     1 Similarity 65.8%; Pred. No. 0.0016; 25; Conservative 4; Mismatches 6;
                                                                                                                      40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 КРААКАААКРААКРААКРААКРААКРА 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 KEYAAAEAK--YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36182, Application US/09864761
Patent No. US20020048763A1
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-864-761-36182
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US-09-820-843A-24
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Sequence 1, Application US 0.00115103A1

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFRENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 2.7
LENGTH: 356
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                                      1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAAEAKKKAKAE----AKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKA-----EKAAKKAEAK--AYKAAEAK-KKAKAEAKKYAK---- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 104.5; DB 10; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.5%; Score 111.5; DB 9; Length 3: Best Local Similarity 40.7%; Pred. No. 0.0043; Matches 44; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 ------AAKAEK----KEYAAAEA-----KYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
CTHER INFORMATION: tola protein
NAME/KEY: misc feature
OTHER INFORMATION: gi|9656364
US-09-820-843A-27
                                                                                                                                                                      180 ATKAAPAK-KAPAKKAATKAA 199
                                                                                                                   55 A--AAEAKYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                      US-09-820-843A-27
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8 EKAYAKKAEKAAKK - - AEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA 65
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                                                                                                                                                                    9
                                                                                                            Query Match 27.9%; Score 102; DB 9; Length 369; Best Local Similarity 43.1%; Pred. No. 0.03; Matches 31; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.0%; Score 99; DB 9; Length 102; 40.5%; Pred. No. 0.015; ive 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KOVESDI, INRE
APPLICANT: BROUGH, DOUGLAS B.
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/101,751
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/700,846
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SSOUTHARE: PATENTING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SSOUTHARE: PATENTING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SSOUTHARE: PATENTING DATE: 1905-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 10, 2003, 12:53:44 Job time : 24.0479 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 90, Application US/09999724; Publication No. US20030022355A1; GENERAL INFORMATION:
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|3322751
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic US-09-999-724-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : :|||| || || ||
64 AEEKRAEAEAAEAAPAA 82
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325 EEARRKEAEFEA 336
                                                                                                                                                                                                                                                                                                                                           66 AKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 32; Conserv
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WS-09-820-843A-95

WS-09-820-843A-95

WS-09-820-843A-95

WWRENT APPLICATION NUMBER: US/09/820,843A

CURRENT APPLICATION NUMBER: US/09/820,843A

WWWREN PILING DATE: 2001-03-30

WUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.0

SEQ ID NO 95

LINCTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAK---KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA---AKAEKKEYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
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28.6%; Score 104.5; DB 10; Length 617;
Best Local Similarity 40.0%; Pred. No. 0.031;
Matches 32; Conservative 18; Mismatches 23; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC005529.7

OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

OTHER INFORMATION: SERFESSED IN BRAIN, SIGNAL = 5.6

OTHER INFORMATION: SMISSPROT HIT: BP445754.1, EVALUE 3.00e-22
                                         PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2000-09-21

PRIOR PELING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SEOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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OTHER INFORMATION: conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: T. pallidum
FEATURE:
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### (OTASU) MAJA 35A9 SIHT

US-08-346-849-16 US-08-23-284A-16 US-09-041-889-38 US-08-167-641C-62 US-08-167-641C-62 US-08-101-751A-62 US-09-101-751A-98 US-09-101-751A-8 US-09-101-751A-8 US-08-113B-3 US-08-344-529-2

Sequence 16, Sequence 38, Sequence 62,

Sequence 4 Sequence 4 Sequence 1

Sequence 62, Sequence 62, Sequence 62, Sequence 90, Sequence 48, Sequence 3, As Sequence 2, As Sequence 54, Sequence 54, Sequence 52, As Seque

Sequence Sequence Sequence Sequence

US-08-557-309B-54 US-08-834-306-52 US-08-993-674A-52

ALIGNMENTS

us-09-816-989a-5.open.rai

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APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESE for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: Unne 5, 1995
CLASSIFTCATION DATA:
PRIOR APPLICATION 1435
PRIOR APPLICATION ADATA:
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERCE/DOCKET NUMBER: 212/066
TELEPENONICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                          ; Sequence 64, Application US/08460890A; Patent No. 5994109; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
TELEX: 67
                                64, Appl

8, Appli

10, Appli

10, Appli

2, Appli

27, Appli

27, Appli

201, Appli

201, Appli

201, Appli

3, Appli

6, Appli

6, Appli

7, Appli

8, Appli

9, Appli
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                                                                          March 10, 2003, 12:15:04; Search time 13.6456 Seconds (without alignments) 166.029 Million cell updates/sec
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                                                                                                                        US-09-816-989A-5
366
1 AKKYAKKEKAYAKKABKAAK......BAKYKABAAKAAAKEAAYBA
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-08-167-641C-64
US-08-462-040-64
US-08-2-040-64
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US-08-2-040-64
US-08-2-040-64
US-08-2-040-64
US-08-2-04-89-2
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-29-28-2
US-09-29-28-2
US-09-29-329-5
US-09-041-889-3
US-08-929-329-5
US-09-041-889-3
US-08-929-329-5
US-09-041-889-3
US-08-929-329-5
US-09-041-889-3
US-08-929-329-5
US-08-929-329-5
US-08-929-444-1
US-08-929-414-1
US-08-929-414-1
US-08-929-414-1
US-08-929-414-1
US-08-939-674A-51
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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158
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144.5
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134.5
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129.5
129.3
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64:

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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                         Sequence 64, Application US/08460971A; Sequence 64, Application US/08460971A; Patent No. 6150168; GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
CTREET: Sulte 4700
                                                                     Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.5%; Score 144.5; DB 4; Length 100;
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US-08-460-971A-64
                                                                                                                                    Indels
                                                              39.5%; Score 144.5; DB 3; ilarity 58.4%; Pred. No. 2.7e-07; Conservative 6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY 1.5.4.

ZIP: 90071-2066

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM SPELICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY,AGENT INFORMATION:
NUMBER: ARCHARGE 3.50
MARE: Marburg 3.50
MARCHARGE 3.50
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REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 212/(
TELECOMMUNICATION INFORMATION:
TELEFHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 100 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                              Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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   US-08-167-641C-64
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moo. Savio L.C.
APPLICANT: Moo. Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristianc, Richard J.
APPLICANT: Cristianc, Richard J.
APPLICANT: Cristianc, Rephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCES: 65
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                  Query Match
39.5%; Score 144.5; DB 2; Length 100;
Best Local Similarity 58.4%; Pred. No. 2.7e-07;
Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                          "Lys Ala" in positions 3 to 100 may be present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
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ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER READABLE FORM:
MEDIUM TYPE: STORAGE
COMPUTER FRANCAGE
COMPUTER PRACEDIC
COMPUTER PRACEDIC
COMPUTER: DATE: DISKETTE, 1.00
SOFTWARE: FRASEE OF WINDOWS 2.0
SOFTWARE: PRACED OF WINDOWS 2.0
SOFTWARE: DATE: DECember 14, 1993
CLASSIFICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 205/012
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
TELEFAX: (7-3510
TELEFAX: 100 mmino acids
STRANDENNESS: SINGLE
TYPE: Amino acid
STRANDENNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08167641C Patent No. 6033884 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear WOLECULE TYPE: peptide FENTURE:
                                                                                              OTHER INFORMATION:
COTHER INFORMATION:
US-08-460-890A-64
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US-08-167-641C-64
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                              1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                      GENERAL INPORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: CHEU, Keiko
ITTLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.6%; Score 134; DB 2; Length 643; ilarity 52.0%; Pred. No. 1.8e-05; Conservative 9; Mismatches 23; Indels
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Patent No. 6228601

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ctchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 99,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           US-08-216-894-8
; Sequence 8, Application US/08216894
; Patent No. 5876734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 643 amino acids
amino acid
                                                                                           59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                     62 АКАКАКАКАКАКАКА 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 TKVÁBÁBKOKÁABÁÁ 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KYKAEAAKAAAKEAA 74
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                 1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
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Э
                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/08462040
| Patent No. 6177554
| GENERAL INFORMATION:
| APPLICANT: Smith, Louis C. APPLICANT: Smith, Louis C. APPLICANT: Gotteniano, Richard J. APPLICANT: Gotteniano, Richard J. APPLICANT: Gottenia, Stephen TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESSE: ADDRESSE: Lyon & Lyon ; STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-462-040-64
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                         23; Indels
58.4%; Pred. No. 2.7e-07; ive 6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PasteSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION S36
PRICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY, AGENT INPORMARTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                          59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                                                                                  62 АКАКАКАКАКАКА 78
                         45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.5
Best Local Similarity 58.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                                                                             US-08-462-040-64
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360 ATKVABAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 416
                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAXAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                               Query Match 35.5%; Score 130; DB 2; Length 472; Best Local Similarity 51.4%; Pred. No. 3.1e-05; Matches 38; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. 0.2.0.0.0.
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K & Lardner
STREET: 3000 K & Lereet, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 472;
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51.4%; Pred. No. 3.1e-05;
tive 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: Washington, D.C.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,746

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-115-746-10
; Sequence 10, Application US/09115746
; Patent No. 6228601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85321
TELECOMMUNICATION INFORMATION:
TELEFPONE: (202)672-5399
TELEFAX: (202)672-5399
                        TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 472 amino acids
amino acid
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Best Local Similarity 51.4
Matches 38; Conservative
                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-216-894-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 TKVAEAEKQKAAEA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KYKAEAAKAAAKEA 73
                                                                                                                                                                                                                linear
                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-115-746-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08216894
; Patent No. 5976734
; GENERAL INFORMATION:
    APPLICANT: Kirchhoff, Louis V.
    APPLICANT: Otsu, Keiko
    TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Foley & Lardner
    STREET: 3000 K Street, N.W., Suite 500
    CORRISTORN ADDRESS:
    ADDRESSES: Soley & Lardner
    STREET: Mashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.6%; Score 134; DB 4; Length 643; Best Local Similarity 52.0%; Pred. No. 1.8e-05; Matches 39; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY 1982

ZIP: 20007-5109

COMPUTER READBLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PACFORIT Release #1.0, Version #1.25
SOFTWARE: PACFORIT Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 24-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746 FILING DATE:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
                           STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 643 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 TKVAEAEKOKAAEAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 KYKAEAAKAAAKEAA 74
                                                                                                       20007-5109
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-216-894-10
                                                                           COUNTRY:
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Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 564;
                                                                                          COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.5%; Score 130; DB 4;
Best Local Similarity 51.4%; Pred. No. 3.7e-05;
Matches 38; Conservative 9; Mismatches 23
                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
       3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/09041889;
Patent No. 6033664
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer:
TITLE OF INVENTION: Diagnosis, Prev
TITLE OF INVENTION: Ulcerative Coli
TITLE OF INVENTION: Microbial UC pA
NUMBER OP SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MR-IN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 90436
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acid
                             Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 TKVAEAEKQKAAEA 518
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CITY: San Diego
STATE: California
                                    COUNTRY: USA
TP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-041-889-27
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                        JUSTICE 21, Application US/08216894

Patent No. 5876734

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Grav, Keiko

ITILE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSES: Foley & Lardner.

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COMPUTRY: USA

ZIP: 20007-5109

COMPUTRY: IBM PC COMPATION:

MEDIUM TYPE: Flopy disk

COMPUTER: Patentin Release #1.0, Version #1.25

CURENT APPLICATION DATA:

ATTORNEY APPLICATION DATA:

ATTORNEY APPLICATION NUMBER: US/08/216,894

FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INPORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

RELEPHONE: (202)672-5399

TELLEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.5%; Score 130; DB 2; Length 564; Best Local Similarity 51.4%; Pred. No. 3.7e-05; Matches 38; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 564 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                    417 TKVAĖAEKOKAAĖA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 TKVAEAEKOKAAEA 518
                                                                      60 KYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KYKAEAAKAAKEA 73
                                                                                                                                                                                                         US-08-216-894-2
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US-09-115-746-2
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58 EAKYKAEAAKAAAKEAAY 75
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                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                            US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-293-284A-2
          US-08-346-849-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                        DB 3; Length 214;
                                                                                                                                                                                                                                                                                                                                      35.4%; Score 129.5; DB 3; Length llarity 45.7%; Pred. No. 1.5e-05; Conservative 4; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNATE: MASBACHUSELES
COUNTRY: U.S.A.

ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUINCE CHARACTERISTICS:

NEWSTERN CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 AAA-----EAKYKAEAAKAAAKEAAYEA 77
               ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9819
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
FILING DATE: 11-APR-1997
                                                                                                                                                                                                           LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NENGTH: 433 amino acids
TYPE; amino acid
                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-346-849-2
                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKA-AKAEK---KEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEB: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
     Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%; Score 123; DB 2; Length 433;
46.2%; Pred. No. 0.00013;
tive 10; Mismatches 28; Indels
                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION NUMBER: 07/973,326
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
Query Match 33.6%; Score 123; DB 1; Best Local Similarity 46.2%; Pred. No. 0.00013; Matches 36; Conservative 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08293284A Patent No. 5955343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 861-6240
                                                                                                                                                                                                                                                350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             58 EAKYKAEAAKAAAKEAAY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 433 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.2
Matches 36; Conservative
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                                                                                                                       Sequence 201, Application US/09095855
Fatent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
UNDBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAABAKKKAKAE----AKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 121; DB 4; Length 223; 55.6%; Pred. No. 9.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATONEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 АТКААРАК-КАРАККААТКАА 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 A--AAEAKYKAEAAKAAAKEA 73
350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.6
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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```

Sequence 201, Application US/09205426 Patent No. 6406704

```
## APPLICANT: Watson, James D.

## APPLICANT: Watson, James D.

## APPLICANT: Tan, Paul L. J.

## TITLE OF INVENTION: Compounds and Methods for Treatment and

## TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

## FILE REFERENCE: 11000-11002-04

## CURRENT PILING THE 1998-06-11

## EARLIER PILING DATE: 1998-06-12

## EARLIER PILING DATE: 1998-06-12

## EARLIER PILING DATE: 1998-06-12

## EARLIER PILING DATE: 1996-08-29

## NUMBER OF SEQ ID NOS: 208

## SOOTHARE: PattSEQ for Windows Version 3.0

## SEQ ID NO 201

## SEC ID NO 201

## SEC ID NO 201

## SEC ID NO 201

## SEQ ```

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```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:15:04; Search time 25.2194 Seconds (without alignments) 327.825 Million cell updates/sec

US-09-816-989A-6 409 1 AKKYAKKEKAYAKKAEKAAK......KKAYKAEAAKAAAKEAAYEA 86 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 2000        | nescribcion |        | tolA protein (impo | probable erythrocy | membrane spanning | membrane spanning | Tola protein PA097 | histone H1 - sea u | histone H1 - Chlam | TolA colicin impor | probable hupB - My | histone H1-beta, e | mst101-1 protein - | outer membrane int | cytosolic repetiti | sperm tail-specifi | histone H1-gamma, | R27-2 protein - Tr | repetitive protein | histone H1 - sea u | outer membrane pro | zuotin - yeast (Sa | histone H1 - rainb | histone H1, gonada | H1.1   | histone H1.10 - ch | hypothetical prote | hypothetical prote |        | histone H1.01 - ch |
|-------------|-------------|--------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|
| SUMMARIES   |             |        |                    |                    |                   |                   |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |        |                    |                    |                    |        |                    |
| SUMMA       | 77          | JV0057 | AG0592             | T09127             | F90725            | G85576            | E83525             | A25550             | 859589             | AC0138             | G70673             | A28100             | 834153             | G64064             | A44993             | S51364             | A26721            | T30296             | E60110             | 809388             | B43592             | S25194             | HSTRIR             | HSUR1P             | T23778 | A28456             | AE1689             | T06636             | T11583 | A23055             |
| 2           | 9 ;         | 7      | ~                  | ~                  | ~                 | N                 | ~                  | N                  | 7                  | N                  | N                  | N                  | ~                  | N                  | ~                  | ~                  | ~                 | N                  | ~                  | ~                  | ~                  | ~                  | Н                  | Н                  | N      | ~                  | ~                  | ~                  | N      | 7                  |
| ,<br>,<br>, | rengen      | 421    | 376                | 1701               | 394               | 394               | 347                | 210                | 231                | 388                | 214                | 211                | 344                | 372                | 328                | 1390               | 217               | 1128               | 219                | 206                | 384                | 433                | 206                | 248                | 208    | 220                | 243                | 924                | 1403   | 218                |
| %<br>Query  | MACCE       | 0      | 38.5               | 38.3               |                   | 37.9              | 37.7               | 36.9               | 36.4               | 36.1               | 35.9               | 35.2               | 34.8               | 34.7               | 34.4               | 34.4               | 33.7              | 33.6               | 33.0               | 32.8               | 32.6               | 32.6               | 32.4               | 32.3               | 32.0   | 31.9               | 31.9               | 31.7               | 31.7   | 31.5               |
| ,<br>,<br>, | acore       | 164    | 157.5              | 156.5              | 155               | 155               | 154                | 151                | 149                | 147.5              | 147                | 144                | 142.5              | 142                | 140.5              | 140.5              | 138               | 137.5              | 135                | 134                | 133.5              | 133.5              | 132.5              | 132                | 131    | 130.5              | 130.5              | 129.5              | 129.5  | 129                |
| Result      | 2           | -      | 01                 | m                  | 4                 | ស                 | 9                  | 7                  | 80                 | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24     | 25                 | 56                 | 27                 | 28     | 29                 |

| hypothetical prote | histone H1 - musco | histone H1-II - Vo | histone H1 (clone | cgcr-4 protein - C | histone H1 (clone | histone H1.02 - ch | histone H1.03 - ch | conserved hypothet | hypothetical prote | histone H1 homolog | histone H1.11L - c | tolA protein VC183 | histone H1B - Afri | histone H1B - Afri | hypothetical prote |
|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T17698             | S01262             | JN0748             | T06241            | S19113             | T06257            | HSCH1              | D28456             | E75383             | T06635             | 861926             | B28456             | A82152             | HSXL1B             | 151447             | T22455             |
| N                  | N                  | N                  | N                 | ~                  | N                 | Н                  | ~                  | ~                  | 0                  | ~                  | ~                  | 7                  | -                  | ~                  | 7                  |
| 311                | 218                | 241                | 284               | 265                | 288               | 218                | 224                | 581                | 606                | 182                | 225                | 356                | 219                | 220                | 581                |
| 31.2               | 30.9               | 30.9               | 30.9              | 30.8               | 30.8              | 30.7               | 30.7               | 30.6               | 30.4               | 30.3               | 30.2               | 30.1               | 30.0               | 30.0               | 30.0               |
| 127.5              | 126.5              | 126.5              | 126.5             | 126                | 126               | 125.5              | 125.5              | 125                | 124.5              | 124                | 123.5              | 123                | 122.5              | 122.5              | 122.5              |
| 30                 | 31                 | 32                 | 33                | 34                 | 32                | 36                 | 37                 | 38                 | 33                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

| RESULT 1                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| tolA protein - 1                                           | 50003/<br>tolA protein - Escherichia coli (strain K-12)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| C; Species: Escherichia coli                               | lerichia coli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| C;Date: U/-Sep-1990 #sequen<br>C;Accession: JV0057; B64810 | C;Date: U/-sep-1990 #sequence_revision U/-sep-1990 #text_cnange U1-mar-2002<br>C;Accession: JV0057; B64810                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| R; Levengood, S.K.; Webster,                               | K.; Webster, R.E.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| A:Title: Nucleot                                           | o. macterior. 1.1, movu-evolv, 199<br>Affitle: Nucleotide sequences of the tolk and tolk genes and localization of their produc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| A; Reference num                                           | A;Reference number: JV0057; MUID:90078104; PMID:2687247                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| A;Accession: JV0057                                        | 10057                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| A;Residues: 1-421 <lev></lev>                              | 21 <lev></lev>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| A; Cross-reference                                         | A,Cross.references: GB:M28232; NID:9148018; PIDN:AAA24683.1; PID:9148019                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| A; Experimental a                                          | Ajäxperimental gource: strain JMIOS.<br>Ajönte- the authore tranglated the initiation codon (370 for regidne 1 ag Val                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| R,Blattner, F.R                                            | R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| .A.; Rose, D.J.; Mau, B.; Sha                              | A.; Rose, D.J.; Mau, B.; Shao, Y.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| A:Title: The cor                                           | molete genome sequence of Escherichia coli K-12.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| A; Reference numb                                          | A; Reference number: A64720; MUID: 97426617; PMID: 9278503                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| A;Accession: B64810                                        | 4810                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| A;Status: nucle                                            | A;Status: nucleic acid sequence not shown; translation not shown                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| A; Molecule type: DNA                                      | S: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| A; Acatologia : 1                                          | A), CESTALL SELVEL SELVEL CONTROL OF THE SELVE OF THE SEL |
| A. Evnerimental                                            | A)-CLOSE TELECITED AND AND AND AND AND AND AND AND AND AN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| C; Comment: tolA                                           | C. Comment: tola and tola proteins are necessary for colicins E2, E3, A, and K to reach the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| C;Genetics:                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| A;Gene: tolA                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| A; Map position: 17 min                                    | 17 min                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| A; Scarc cocon:                                            | Gold<br>Golds Friedler T learn transmission                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| F:14-34/Domain:                                            | C;Acywords: nucleociae binaing;Loop; Lealmamminiane process<br>R=14.14.14/Domain: transmemhrane Heratus predicted AMSS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| F;78-301/Domain                                            | : helical #status predicted <pre></pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| F;355-362/Region                                           | n: nucleotide-binding motif A (P-loop)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Query Match                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Best Local Similarity Matches 51: Conserv                  | 59.3%; Pred. No. 4.8e-05; ative 7: Mismatches 18:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|                                                            | 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Qy 7 KEKAYI                                                | KEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEA 59                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Db 148 KAEAD                                               | KAEADAKAAEEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAAALKKKAEAAEAAAAEA 207                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Qy 60 KYKA-                                                | 60 KYKAEAAKKAYKAEAAKAAAKEAA 83                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| c                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| DD 208 RKKAA                                               | RKKAATEAAEKA-KAEAEKKAAAEKA 232                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

RESULT 2 AG0592

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Toll protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
Toll protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83525
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
   A,Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09
A,Experimental source: strain 0157:H7, substrain EDL933
  D.J.; Mayhew
K.; Apodaca,
   membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-34 <HRA>
A;Cesidues: 1-34 <HRA>
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:gl3360233; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
   C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001
C;Accession: G85576
F;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
  16; Gaps
  1 AKKYAKKEKAYA----KKAEKAA----KKAEAKAYKAAEAKKKAKAEA----KKYAKAA 47
  16; Gaps
   1 AKKYAKKEKAYA----KKAEKAA----KKAEAKAYKAAEAKKKAKAEA----KKYAKAA 47
   ch 37.9%; Score 155; DB 2; Length 394; al Similarity 53.1%; Pred. No. 0.0002; 51; Conservative 6; Mismatches 23; Indels 1
  Length 394;
   Score 155; DB 2; Length 39
Pred. No. 0.0002;
6; Mismatches 23; Indels
   227 AAEK---AAADKKAAAEKAAADKKAAAAKAAEKAA 259
   48 KAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
   48 KAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
   Query Match
Best Local Similarity 53.1%;
Matches 51; Conservative
  Best Local Similarity
Matches 51; Conserv
   A; Residues: 1-394 <STO>
   A, Status: preliminary A, Molecule type: DNA
  A; Accession: G85576
  A; Accession: F90725
   A; Gene: EC80774
  Query Match
   A;Gene: tolA
   Genetics:
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                                      C; Species: Salmonella enterica subsp. enterica serovar Typhia
A; Note: this species has also been called Salmonella typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C; Accession: AG0592
R; Parkhill, J: Dougan, G: James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J:; Churcher, th, T: Connerton, P: Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
A; Residues: 1-376 <PAR>
A; Residues: 1-376 <PAR>
A; Residues: 1-376 <PAR>
A; Residues: 1-376 <PAR>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
             protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
  membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F90725
  probable erythrocyte-binding protein NAEBL - Plasmodium yoelii
C:Species: Plasmodium yoelii
C:Species: Dlasmodium yoelii
C:Accession: T03127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1938
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Accession: T09127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Besidues: 1-1701 <KAP>
A;Experimental source: Subspecies yoelii; strain YM
C:Genetics:
A;Gene: maebl
A;Introms: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
  5
  9
  Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYA----KAAKAEKKEYA 55
  Gaps
   1 AKKYAKKEKAYA---KKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAAK---- 48
   Query Match
38.5%; Score 157.5; DB 2; Length 376;
Best Local Similarity 54.8%; Pred. No. 0.00013;
Matches 51; Conservative 10; Mismatches 17; Indels 15;
   19;
  DB 2; Length 1701;
   18; Indels
   Score 156.5; DB 2.
Pred. No. 0.00047;
9; Mismatches 18
  49 AEKKEYAA--AEAKYKAEAAKKA----YKAEAAKAAAKE 81
  185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 217
  56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
   Match 18.3%;
Local Similarity 53.5%;
les 53; Conservative
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Query Match Matches

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36.1%;
  Query Match
Best Local Similarity 45.2
Matches 47; Conservative
  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
  A, Molecule type: DNA
   C; Accession: AC0138
  Query Match
   A;Gene: tolA
   Best Loca
Matches
   C; Genetics:
  25
  RESULT 10
   RESULT 9
  8
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   System of the Chlamydomonas reinhardtii histone H1 - Chlamydomonas reinhardtii chstone H1 - Chlamydomonas reinhardtii chstone H1 - Chlamydomonas reinhardtii chstone H1 - Chare: L10-Mpr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999 Chacession: S59589; S62122 Fervision 19-Apr-1996 #text_change 23-Jul-1999 Chacession: S59589; S62122 Fervision 19-Apr-1996 #text_change T.; Schmitt, R. Curr. Genet. 28, 333-345, 1995 Apr-1995 Apr-1996 Fervision Structure and regulatory elements of Chlamydomonas histone gen Areference number: S59581; MUID:96120862; PMID:8590479
  A; Residues: 1-231 <FAB>
A; Cross-references: EMBL:U16726
A; Cross-references: EMBL:U16726
A; Note: the authors did not translate the codon for residue 1
B; Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R. submitted to the EMBL Data Library, October 1994
A; Description: The organization, structure and controlling elements of Chlamydomonas his A; Reference number: S62122
   A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: tolA; PA0971
  a
   A25550

A25550

A25550

C; Species: Lytechinus pictus)
C; Species: Lytechinus pictus (painted urchin)
C; Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C; Accession: A25550
R; Moucleic Acids Res. 14, 8121-8133, 1986
A; Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus a A; Reference number: A25550; MUID:87040778; PMID:3022245
A; Accession: A2550
A; Molecule type: DNA
A; Residues: 1-210 eKNO>
A; Residues: 1-210 eKNO>
A; Residues: 1-210 eKNO>
A; Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C; Superfamily: histone H1
C; Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
   4;
   3,
   120 ARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDAKKKAAEDA 179
  Gaps
   Gaps
  2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEAK 60
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAA------EAKKKAKAKAEAKKYA---- 44
  22;
  Length 347;
   Length 210;
   21, Indels
  Query Match 36.9%; Score 151; DB 2; Length 210 Best Local Similarity 51.7%; Pred. No. 0.00024; Matches 46; Conservative 10; Mismatches 25; Indels
   45 --KAAKAEKKEYAAAEAKYKA--EAAKKAYKAEAAKAAAKEAA 83
   37.7%; Score 154; DB 2;
47.6%; Pred. No. 0.00021;
tive 11; Mismatches 21;
  61 YKAE-----AAKKAYKAEAAKAAAKEAA 83
  A;Accession: 559589
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
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Best Local Similarity 47.6*
Matches 49; Conservative
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
  A; Molecule type: DNA
   A;Accession: S62122
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R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I. Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
   C; Accession: G70673

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, N.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Kajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Squares, R.; Sullston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome shakeference number: A70500; MUID:98295987; PMID:9634230
   A;Residues: 1-214 <CCL>
A;Cross-references: GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05427.1; PID:g1694845
A;Experimental source: strain H37Rv
   2
  3,
  TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
   A;Cross-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
   probable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480 C;Genetics: A;Intrones: 62/3; 101/3 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome
  103 AKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKAEKKPKKEGEKKKAAKPAKAEK 162
   1 AKKYAKKEKAYAKKAEKAAKKAEA------KAYKAAEAKKKAKAEAKKYAKAAEK 51
  -AEAKYKAEAAKKAYKAEAAKAAAKEAA
  27;
   Length 388;
   Length 231;
   29; Indels
  Indels
  7 KEKAYAKKAEKAAKKAEAKAYK----AAEAKKKAKAEAKKYAKAAKAEKKE
  215 EVAEKAAADAAEKKAAADAEKKAAAAKKVAAAAEAKKKAAAAEAA 258
   54 ------YAAAEAKYKAEAAKK-AYKAEAAKEAA
   DB 2;
  21;
   36.4%; Score 149; DB 2; Local Similarity 39.5%; Pred. No. 0.00035; les 47; Conservative 7; Mismatches 29,
   Score 147.5; DB 2
Pred. No. 0.00067;
9; Mismatches 21
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Local Similarity
   Local Similarity
   A;Gene: tolA
A;Start codon: GTG
   49;
  Query Match
  Query Match
  C; Genetics
   Matches
   RESULT 14
  A44993
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  RESULT 12
534153
metalol_1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Species: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34153
A;Reference number: S34153
A;Reference number: S34153
A;Reteus: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 «NEE>
A;Cross-references: EMBL:X73480; NID:g313199; PID:g313200
  65 AKK--EKEAAEKKCAEAAKKEKEAAEKKCAEAAKKEKEAAEKKCAEAAKKKCAEAAEK 122
  Gaps
   Gaps
   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEAK 60
  AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAK--AEAKKYAKAKAE----- 50
   1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAEKKEY
   10;
  4
   34.8%; Score 142.5; DB 2; Length 344; llarity 48.0%; Pred. No. 0.0014; Conservative 7; Mismatches 23; Indels 23
   Length 214;
  35.2%; Score 144; DB 2; Length 211; 53.6%; Pred. No. 0.00074; ive 6; Mismatches 29; Indels
   34; Indels
                                      Score 147; DB 2;
Pred. No. 0.00046;
3; Mismatches 34;
  169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
  55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  Cross-references: PlyBase:FBgn0011816; Superfamily: neurofilament triplet H protein
  61 YKAEAAKKAYKAEAA-KAAAKEAA 83
  35.9%;
   Best Local Similarity 53.6
Matches 45; Conservative
   Conservative
   A; Gene: FlyBase: Dhyd/mst101
A,Gene: hupB
C,Superfamily: histone H1
                                      Query Match
Best Local Similarity
Matches 47; Conserv
   Local Similarity
nes 49; Conserv
   Query Match
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Matches 49
  Query Match
  C, Genetics
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A,Cross-references: GB:U32722, GB:L42023, NID:g1573348, PIDN:AAC22041.1; PID:g1573353; TJI R;Sen, K.; Sikkema, D.J.; Murphy, T.F. Gene 178, 75-81, 1996
A,Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and A,Reference number: JC5212; MUID:97080550; PMID:8921895
   A,Accession: JC5212
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-2
  Cypeolic repetitive antigen - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
R;Lafaille, J.J.; Lines, J.; Krieger, M.A.; Souto-Padron, T.; de Souza, W.; Goldenberg, S;
NOI. Biochem. Parasitol. 35, 127-136, 1989
A;Fitle: Structure and expression of two Trypanosoma cruzi genes encoding antigenic prote:
A;Reference number: A44993; MUID:89364992; PMID:2475776
A;Recossion. A44993
A;Ratus: preliminary; not compared with conceptual translation
A;Residues: J-328 A.BAP
A;Coss-references: GLAP>
A;Cross-references: GLAP>
A;Cross-references: GLAP>
C;Superfamily: neurofilament triplet H protein
   Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1958 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64064; JC5212
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, P.D.M.; Brandon, R.C.; Frine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: G64064
   ņ
   <u>ب</u>
   Gaps
   Gaps
   1 AKKYA----KKEKAYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAKKEK 51
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA-EKKEYAAAEA 59
   14;
   2,
  A) Experimental source: strain 1479
A, Note: the authors translated the codon CGT for residue 190 as Ala
   Length 328;
  A,Status: nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-372 <TIGR>
  Length 372;
   22; Indels
   Indels
123 KKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKE 164
   34.4%; Score 140.5; DB 2; 50.0%; Pred. No. 0.0018; cive 11; Mismatches 28;
  34.7%; Score 142; DB 2;
52.1%; Pred. No. 0.0016;
iive 9; Mismatches 22
   KEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
   Matches 44; Conservative
   Conservative
  A; Cross-references: GB: U32470
```

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Spinse rail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
S; Blochem. 25, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe
A;Teile: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe
A;Teile: Tandemly arranged repeats of a novel highly charged of Drosophila hydei.
A;Recence number: S31364, MUID:95045538; PMID:7957199
A;Accession: S51364
A;Accession: S51364
A;Accession: S3164
A;Cross-references: EMBL:X73481
R;Nesesion: S34154
A;Reference number: S34154
A;Reference number: S34154
A;Accession: S34154
A;Acce
  ŝ
24; Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAE 58
  Query Match

34.4%; Score 140.5; DB 2; Length 1390;
Best Local Similarity 46.2%; Pred. No. 0.0055;
Matches 48; Conservative 9; Mismatches 23; Indels 24;
  167 TKVAEAEKQKAAEATKVAEAEKQKAAEA 194
  60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
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Search completed: March 10, 2003, 12:28:29 Job time : 26.2194 secs

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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 19.5949 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-816-989A-6 409 1 AKKYAKKEKAYAKKAEKAAK.......KRAYKAEAAKAAAKEAAYEA 86

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | P19934 escherichia | P50600 pseudomonas | P06144 Tytechinus | P95109 mycobacteri |           | Q08695 drosophila |            |           |            |          | aedes     | aedes     | Q9zhc5 mycobacteri | P29720 treponema p |            |          |          |           | -          |            | _          |           |          | volvox    | gallus   | gallus     | gallus     | xenopus | P40278 chironomus | P27806 triticum ae | ĭ    | _     | P40276 chironomus |
|-----------|----------------|--------------------|--------------------|-------------------|--------------------|-----------|-------------------|------------|-----------|------------|----------|-----------|-----------|--------------------|--------------------|------------|----------|----------|-----------|------------|------------|------------|-----------|----------|-----------|----------|------------|------------|---------|-------------------|--------------------|------|-------|-------------------|
| SUMMARIES | ID             | TOLA ECOLI         | TOLA PSEAE         | H1_LYTPI          | DBH MYCTU          | DBH_MYCBO | MST1 DROHY        | TOLA HAEIN | H1B STRPU | MST2_DROHY | HIGSTRPU | RS6_AEDAE | RS6_AEDAL | DBH_MYCSM          | TMPB TREPH         | ZUO1_YEAST | H1 ONCMY | H1_PARAN | H11_CAEEL | H110_CHICK | YDF3_SCHPO | H101_CHICK | ASR_KLEPN | H1_ANAPL | H12_VOLCA | H1_CHICK | H103_CHICK | HIIL_CHICK |         | HIE_CHITE         | H1_WHEAT           |      |       | H1B_CHITE         |
|           | DB             | -                  | -                  | -                 | -                  | -         | ,                 | н          | Н         | Н          | П        | -         | -         | н                  | ч                  | ч          | ч        | -        | Н         | П          | Ч          | П          | П         | 7        | ч         | -        | 7          | ч          | ч       | -                 |                    | н    | -1    | Н                 |
|           | Length         | 421                | 347                | 210               | 214                | 202       | 344               | 372        | 211       | 1391       | 217      | 346       | 349       | 208                | 384                | 433        | 206      | 248      | 207       | 219        | 1403       | 218        | 139       | 217      | 240       | 217      | 223        | 224        | 219     | 237               | 238                | 225  |       | 232               |
| d         | Query<br>Match | 40.1               | 37.7               | 36.9              | 'n.                | ď.        | 34.8              | 34.7       | 34.5      | 34.4       | 33.7     | 33.6      | 33.5      | 33.4               | 32.6               | 32.6       | 32.4     | 32.3     | 32.0      | 31.9       | 31.7       | 31.5       | 31.1      | 30.9     | 30.9      | 30.7     | 30.7       | 30.2       | 30.0    | 29.7              | 29.7               | 29.6 | 29.5  | 29.3              |
|           | Score          | 164                | 154                | 151               | -                  | 146.5     | 142.5             | 142        | 141       | 140.5      | m        | 137.5     | 137       | 136.5              | 133.5              | 133.5      | 132.5    | 132      | 131       | 130.5      | 129.5      | 129        | 127       | 126.5    | 126.5     | 125.5    | 125.5      | 123.5      | 122.5   | 121.5             | 121.5              | 121  | 120.5 | 120               |
|           | Result<br>No.  | +                  | 7                  | ო                 | 4                  | S         | v                 | 7          | æ         | σ          | 10       | 11        | 12        | 13                 | 14                 | 15         | 16       | 17       | 18        | 19         | 20         | 21         | 22        | 23       | 24        | 22       | 26         | 27         | 28      | 29                | 30                 |      | 32    | 33                |

| P19649 treponema p<br>P02254 salmo trutt<br>P0888 gallus gall<br>P40277 chironomus<br>Q07134 chironomus<br>P10713 chironomus<br>P57873 pasteurella<br>P57873 pasteurella<br>P57873 pasteurella<br>P57873 galturella<br>P15865 xenopus lae<br>P10867 drosophila |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| TWPB TREPA<br>H1 SALTR<br>H11R CHICK<br>H1C CHITE<br>H10_CHITH<br>H14 HUMAN<br>H11_GLYSA<br>IF2_PASMU<br>H1A XENLA<br>H10_T XENLA<br>H11_GLYBA<br>H11_GLYBA                                                                                                    |
| <b>нанананана</b>                                                                                                                                                                                                                                              |
| 325<br>221<br>221<br>221<br>221<br>203<br>233<br>233<br>233<br>233                                                                                                                                                                                             |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                         |
| 120<br>118.5<br>118<br>118<br>118<br>117<br>116.5<br>115.5<br>115.5                                                                                                                                                                                            |
| 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                        |

### ALIGNMENTS

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MEDLINE=97113525; PubMed=8955385;
  49;
   REVISIONS
   TRANSMEM
   SEQUENCE
  Query Match
   Local
  DOMAIN
   Matches
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   4.
   Gaps
  MEDLINE-99312679; PubMed-110404600; Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; Flueckthun B., Wlodawer A.; Flueckthun B., Wlodawer A.; Flueckthun B., Wlodawer A.; Flueckepton: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999) GETUCLINE 7:711-722(1999) THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, El, El, El, El, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.

-! SIBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
  7 KEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA-----KAEKKEYAAAEA 59
  AND LAMB. -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
   Pransport; Protein transport; Bacteriocin transport; Transmembrane;
   10 X TANDEM REPEATS OF [ED]-K(1,2)-
  10;
           "TolA central domain interacts with Escherichia coll porins."; EMBO J. 15:6408-6415(1996).
  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
  40.1%; Score 164; DB 1; Length 421; 59.3%; Pred. No. 2.5e-05;
  18; Indels
  Transport; Frocess commissions; 3D-structure; Complete proteome. nomain 1 13 CYTOPLASMIC (POTENTIAL).
  PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
   (2,4).
8B2F52B4B97C655E CRC64;
  X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
   01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
  347 AA
   7; Mismatches
   208 RKKAATEAAEKA-KAEAEKKAAAEKA 232
   60 KYKA--EAAKKAYKAEAAKAAKEAA 83
  EMBL; M28232; AAA24683.1; -.
EMBL; AE000177; AAC73833.1; -.
EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
  421 AA; 43156 MW;
  Conservative
  STANDARD;
  PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
  34
421
310
421
278
   Pseudomonas aeruginosa.
   Similarity
   SEQUENCE FROM N.A.
  Tola protein.
TOLA OR PA0971.
   NCBI_TaxID=287;
   PIR; JV0057;
PDB; 1TOL; 20
   RESULT 2
TOLA PSEAE
ID TOLA PSEAE
P5060;
OCT-199'
Lloubes R.;
  Pseudomonas
   STRAIN=PAO;
   51;
  TRANSMEM
  SEQUENCE
  Query Match
Best Local S
  DOMAIN
   DOMAIN
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   Best Loca
Matches
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
  Lytechinus pictus (Painted sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
  Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAA------EAKKKAKAKAKAKA---- 44
  Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.C., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PMO1, an
   EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
   (BY SIMILARITY).
  -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
   22;
                             ğ
   Length 347;
   21; Indels
Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes
   Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
   17 37 POTENTIAL.
38 347 PERIPLASMIC (POTENTIAL).
209 216 POLY-ALA.
347 AA; 37935 MW; EEDD4B04AAQ95945 CRC64;
   180 KKKAAEEAKKKAAAEAAKKKAAVEAAKK--KAAAAAAARKAA 220
  CYTOPLASMIC (POTENTIAL)
   --KAAKAEKKEYAAAEAKYKA--EAAKKAYKAEAAKAAAKEAA
  Score 154; DB 1;
Pred. No. 0.00011;
  HI_LYTPI
AC POG_144,
DT 01-JAN-1988 (Rel. 06, Created)
DT 10-JAN-1988 (Rel. 06, Last sequence update)
DT 10-JAN-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last minimum update)
DF 15-JUL-1999 (Rel. 38, Last minimum update)
DF 16-JUL-1999 (Rel. 38, Last minimum update)
  11; Mismatches
  SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAOl;
MEDLINE=20437337; PubMed=10984043;
   Bacteriol. 178:7059-7068(1996)
  37.7%;
  EMBL; U39558; AAC44660.2; -.
EMBL; AE004530; AAG04360.1; -
  opportunistic pathogen.";
Nature 406:959-964(2000).
  Conservative
  TO N-TERMINUS.
  Pseudomonas aeruginosa.
  16
37
347
216
  Similarity
   Complete proteome. DOMAIN 1
   SEQUENCE FROM N.A.
  (Potential).
  Lytechinus.
NCBI_TaxID=7653;
   PAC OCC OSE DIT
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SEQUENCE FROM N.A.
  IIGR; MT3064;
   STRAIN=H37Rv;
   Bishai W.;
  Query Match
  Matches
   DBH_MYCBO
  RESULT 5
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   8
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   3;
  MEDLINE=9825987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
   HISSP, P02259; IHST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam, PF00538; Ilnker histone; I.
SPROPOM; PD000373; Linkerhist N. 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
   Gaps
   2 KKYAKKEKAYAKKAEKAAKKABAKAYKAABAK-KKAKABAKKYAKAKAKKEYAAABAK 60
   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-GT-2001 (Rel. 40, Last sequence update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa laminin-2-binding protein)
HWP OR HLP OR LBP21 OR WY9986G OR WT3064 OR WTCY349.01.
Mycobacterium tuberculosis
  Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                    MEDLINE=87040778; PubMed=3022245;
Knowles J.A., Childs G.J.;
Knowles J.A., Childs G.J.;
"Comparison of the late #1 histone genes of the sea urchins
Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986).
-!- FUNCTION: HISTONES #1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLESOSME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELJULAR LOCATION: Nuclear.
-!- SUBCELJULAR LOCATION: Nuclear.
   8,
   Length 210;
  25; Indels
  36.9%; Score 151; DB 1;
51.7%; Pred. No. 0.00012;
tive 10; Mismatches 25;
  214 AA
  155 КРАККААККРААККААККРАККРАККАА 183
  61 YKAE-----AAKKAYKAEAAKAAAKEAA 83
  PRT;
  EMBL; X04488; CAA28177.1; -.
   Conservative
  STANDARD;
  PIR; A25550; A25550.
  Local Similarity
   SEQUENCE FROM N.A.
   STRAIN=H37Rv
   46;
  DBH MYCTU
   Query Match
   Matches
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
   Savita P.,
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILLEE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
   111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
   35.9%; Score 147; DB 1; Length 214;
50.0%; Pred. No. 0.00023;
tive 3; Mismatches 34; Indels 10; Gaps
   DBH WYCBO STANDARD; PRT; 205 AA.

09XB18; Q9S5J5;
16-OCT-2010 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 40, Last amonotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
HUP OR HLP OR MDP1.
Mycobacterium bovis.
Mycobacterium, Actinobacteria; Actinobacteriaceae; Mycobacterium.
NCCBI_TAXID=1765;
   1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
  "Whole genome comparison of Mycobacterium tuberculosis clinical and
   Pragad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
  Pfam; PF00216; Bac_DNA_binding; 1.
PRINTS; PR00624; HISTONEHS.
Probom; PD000945; Bac_DNAbind; 1.
SWART; SM00411; BHL; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
DNA-Dinding; DNA condensation; Repeat; Complete proteome.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOWAIN.
DOMAIN 101 214 DEGENERATE REPRATS REGION.
SEQUENCE 214 AA; 22187 MW; CB09AF20FB353544 CRC64;
   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
  169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
  55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  or send an email to license@isb-sib.ch).
  Tuberculist; Rv2986c; -. InterPro; IPR000119; Bac DNAbind. InterPro; IPR001386; Histone HI/H5.
   [3]
SEQUENCE OF 71-86, AND DNA-BINDING.
  EMBL; Z83018; CAB05427.1; -.
EMBL; AE007127; AAK47393.1; -.
HSSP; P02346; 1HUU.
   Local Similarity 50.09
nes 47; Conservative
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MEDLINE=94200512; PubMed=8150205;
   NCBI_TaxID=727;
   Tola protein.
TOLA OR HI0383
  TOLA HAEIN
  Query Match
  TOLA_HAEIN
  Matches
   RESULT 7
  $444444666666666666666666444488
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   ACCOCCOS DITAL REPORT OF THE R
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   4
   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
  Gaps
  Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
  111 AKKVAK--KAPAKKATKAAKKAATK----APAKKAATKAPAKKAVKATKSPAKKVTKAVK 164
   MSTI01(1).
Drosophila hydei (Fruit fly).
Brosophila hydei Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Metazoa; Arthropoda; Endopterygota; Diptera; Brachycera;
Insecta; Pterygota; Neopera; Endopterygota; Drosophila.
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKA-KAEAKKYAKAAKAEKKEYAAAEA 59
  STRAIN=BCG / Tokyo;
Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth
  REMBL; ABULSTATION REMBL; ABULSTATION RESEPT POUSAGE, INTUT.
R INTERPROF IPRO001386; Histone H1/H5.
R Pfan; PF000161; Bac DNA binding; 1.
DR PRO000624; HISTONE H15.
DR PROSTIF; PS00045; HISTONE LIKE; 1.
DR PROSTIF; PS00045; HISTONE LIKE DOMAIN.
DNA-binding; DNA condensation; Repeat.
BACTERIAL HISTONE-LIKE DOMAIN.
  9
   DB 1; Length 205;
   35.8%; Score 146.5; DB 1; Length ilarity 53.9%; Pred. No. 0.00024; Conservative 3; Mismatches 29; Indels
  DEGENERATE REPEATS REGION.
A -> T (IN REF. 2).
19FCE67885DFE6A8 CRC64;
  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mstl01(1).
  344 AA.
  SEQUENCE FROM N.A., AND CHARACTERIZATION
   165 KTAVKASVRKAATKAPAKKAAAKRPATKA 193
  60 K--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
   PRT;
  EMBL; AB013441; BAA78330.1; -.
  199 199 A
205 AA; 21262 MW;
  EMBL; Y18421; CAB46493.1;
   STANDARD;
  from Mycobacterium.";
  Local Similarity
                     FROM N.A.
   SEQUENCE FROM N.A.
  TISSUR-Testis;
  48;
  STRAIN=AN5;
   DROHY
                     SEQUENCE
  CONFLICT
  Query Match
   MST1 DR
Q08695;
   MST1_DROHY
  Matches
   RESULT 6
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   5
  "Whole-genome random sequencing and assembly of Haemophilus influenzae
Neesen J., Buenemann H., Heinlein U.A.;
"The Drosophila hydei gene.Dhmstill(!) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant flies.";
  Q
   Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAK--AEAKKYAKAKAE----- 50
   SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Milline A.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
   Dev. Biol. 162:414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
   23;
   -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS
  Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
  DB 1; Length 344;
  AND
  ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES
  34.8%; Score 142.5; DB 1; Length 48.0%; Pred. No. 0.00069; tive 7; Mismatches 23; Indels
  123 ККСАЕААККЕКЕААЕКККСАЕААККЕКЕААЕКККСАЕААККЕ 164
   81
   51 -----KKEYAAAEAKYKAEAAKK----AYKAEAAKAAAKE
   P44678; P94810;
01-NOV-1995 (Rel. 32, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
10-LON-2002 (Rel. 41, Last annotation update)
   372 AA
   EMBL, X73480; CAA51875.1; -.
PIR, S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
   PRT;
   Conservative
  Science 269:496-512(1995)
  STANDARD;
   SPERMATID BUNDLES.
   Local Similarity
es 49; Conserv
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Local S...
45;
   DROHY
   SEQUENCE
   Query Match
  MST2_DROHY
   Matches
  RESULT 9
  셤
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   ů,
   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
  Gaps
  1 AKKYA-----KKEKAYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAEK 51
  Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                         22; Indels 14;
  Length 372;
   -> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
  (IN STRAIN 1479).
(IN STRAIN 1479).
(IN STRAIN 1479).
   CYTOPLASMIC (POTENTIAL)
   PERIPLASMIC (POTENTIAL)
  (IN STRAIN 1479)
   Score 142; DB 1;
Pred. No. 0.0008;
   (Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 38, Last annotation update)
  215 KAKAAAEAKAKADAEAKA--ATEAKRKADQASLD 246
   211 AA
  9; Mismatches
   52 KEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
   4 K
  PRT;
  ^ ^ ^ ^ ^ ^ ^
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                  MEDLINE=97080550; PubMed=8921895;
   MEDLINE=88246461; PubMed=2837660;
  Histone H1-beta, late embryonic.
   39831 MW;
   EMBL; U32722; AAC22041.1; -.
EMBL; U32470; AAC44596.1; -.
HSSP; P19934; ITOL.
  34.7%;
52.1%;
  Conservative
  STANDARD;
   234
254
254
306
333
  333
372 AA;
   Strongylocentrotus.
  Query Match
Best Local Similarity
   Complete proteome.
FROM N.A.
   SEQUENCE FROM N.A.
   (Potential).
  NCBI_TaxID=7668;
  TIGR; HI0383; -
   01-APR-1990
01-APR-1990
   15-JUL-1999
   49;
  STRPU
SEQUENCE
  TRANSMEM
   SEQUENCE
   VARIANT
  VARIANT
   VARIANT
   VARIANT
  VARIANT
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  -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
Lai Z.-C., Childs G.; "Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype HI-beta of the sea urchin
   96 KSDAQKAPDAAKKAKLAAKKKBAKEKKAARSKAKKEKLAAKKASK--KTTKKVKKPAAKK 153
  Gaps
   KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEAK 60
   MST101(2).

Drosophila hydei (Fruit fly).

Bukaryota; Matazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Bukaryota; Metazoa; Arthropoda; Mopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7224;
   Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
   SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=95045538; PubMed=7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dhmst101 form extended
alpha-helical rods within the extremely elongated spermatozoa of
   4;
  -1- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
   34.5%; Score 141; DB 1; Length 211; 53.6%; Pred. No. 0.0006;
  30; Indels
  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
   PRT; 1391 AA.
  5; Mismatches
   Eur. J. Biochem. 225:1089-1095(1994)
-1- FUNCTION: POSSIBLE STRUCTURAL RO
  HSSP, P02259, 1HST.
InterPro, IPR001386, Histone H1/H5.
InterPro, IPR003216, Linkerhist N.
Prom, PF00538, linker histone, I.
ProDom, PD000373, Linkerhist N.
SWART; SM00526, H15, I.
   154 АККРААККААККРААККРААККАА 177
  YKAEAAKKAYKAEAA-KAAAKEAA 83
  EMBL; M20314; AAA30052.1; -. PIR; A28100; A28100.
   Conservative
   STANDARD;
  Drosophila hydei.";
  Similarity
  SPERMATIDS.
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Query Match
   Q9U761;
   185
   Matches
  Best Loc
Matches
   RESULT 12
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   5.
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  1196 AKK--EQEPAEMKKCEEAAKKEKERAAEKÇKCAKAAKKEKERAEK-KKCAEAAKKEGEAAE 1252
  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
Histone H1-agama, late.
Strongylocentrous purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
  Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAE 58
  SEQUENCE FROM N.A.
MEDLINE=87172742; PubMed=3031476;
Knowles J.A., Lai Z.-C., Childs G.J.;
"Isolation, characterization, and expression of the gene encoding the histone subtype H1-gamma of the sea urchin Strongylocentrotus
  24;
   QF
   34.4%; Score 140.5; DB 1; Length 1391; 46.2%; Pred. No. 0.0029; Live 9; Mismatches 23; Indels 24;
   1253 KKKCABAAKKEKBAEKKRKCEKAEKAALKRQCAKLVIRAKBAA 1296
  59 AKYKAEAAKKAYKAE-----AAKAA------AKEAA 83
   SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
   PIR; S34154; S34154.
FlyBase; FBgn0020733; Dhyd\mst101(2).
  HSSP, P02259, IHST.
InterPro; IPR001366, Histone H1/H5.
InterPro; IPR002316, Linkerhist N.
Mean, PP00538; linker histone; I.
Probon, PD000373; Linkerhist N. 1.
SWART, SW00526; H15; 1.
   EMBL; X73481; CAA51876.1; -.
   EMBL; M16033; AAA30059.1; -.
  48; Conservative
   STANDARD;
  PIR; A26721; A26721.
  Local Similarity
  Strongylocentrotus.
NCBI_TaxID=7668;
REPEATS
   H1G STRPU
P07796:
  Query Match
  Matches
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  7
   4
   "Aedes mosquitoes ribosomal protein S6 cDNA.";
Submitted (MAY-1999) to the EMBL/GenBank/DDB databases.
-!- FUNCTION: MAY PLAY AN IMPORTANT-ROLE IN CONTROLLING CELL GROWTH
AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
   Gaps
   Aedes aegypti (Yellowfever mosquito).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Prerygota, Neoptera, Endopterygota, Diptera, Nematocera,
Culicoidea, Aedes.
NCBI_TaxID=7159;
   Gaps
  2 KKYAKKEKAYAKKAEK------AAKKAEAKAYKAAEAKKKAKAKAEKYAKAAKA 49
   1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKAAEAKK-KAKAEAKKYAKAAKAEKK-EYAAA 57
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
  CLASSES OF MRNA (By similarity).
--- PTM: Ribosomal protein S6 is the major substrate of protein kinases in eukaryote ribosomes (By similarity).
--- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
   14;
   2.
  DB 1; Length 346;
   217;
  30; Indels
   Indels
   Ribosomal protein; Phosphorylation.
SEQUENCE 346 AA; 39365 MW; 599CFF7B22BD8DFC CRC64;
  33.6%; Score 137.5; DB 1;
llarity 51.1%; Pred. No. 0.0016;
Conservative 5; Mismatches 33;
  Score 138; DB 1;
Pred. No. 0.00099;
   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein 86.
  33.7%; Sco...
46.2%; Pred. No. v...
6; Mismatches
   346 AA
   50 EKKEYAAAEAKYKAEAAKKAYKAEAAKAAKEA 82
   315 PAVAKKEAPKR--KPEAAKGDASAAKKE 340
  82
   EMBL; AF154067; AAF04790.1; -.
InterPro; IPR001377; Ribosomal S6E.
Pfam; PF01092; Ribosomal S6e; I.
ProDom; PD003460; Ribosomal S6E; I.
PROSITE; PS00578; RIBOSOMAL S6E; I.
   PRT;
  58 EAKYKAEAAKKAYKAEAAKAAAKEAAYE
   SEQUENCE FROM N.A.
   43; Conservative
   STANDARD;
   Query Match
Best Local Similarity
   Local Similarity
nes 45; Conserv
  RS6 AEDAE
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TREPH
  SEQUENCE
  Query Match
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  between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  4
  This SWISS-PROT entry is copyright. It is produced through a collaboration
   Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
  255 AKKVAKKEAKKEVKKVTEAAKKADAKAAKAKVEPKKADKKSADSGKKATAGDKKEKKVEK 314
   8; Gaps
  1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKA----AEAKKKAKAEAKKYAKAAKAEKK-EY 54
   Bacteria, Actinobacteria, Actinobacteria (class); Actinobacteridae;
   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
   STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
Lee B.H., Murugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium smegmatis.";
   kinases in eukaryote ribosomes (By similarity).
SIMILARITY: BELONGS TO THE SEE FAMILY OF RIBOSOMAL PROTEINS.
  Score 137; DB 1; Length 349;
Pred. No. 0.0017;
5; Mismatches 33; Indels
  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
  Ribosomal protein; Phosphorylation.
SEQUENCE 349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
    349 AA
  315 KAAPAAKKEAPKR--KPEAAKGDASAAKKE 343
  55 AAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
   Pfam, PF01092, Ribosomal_S6e, I.
ProDom, PD003460, Ribosomal S6E, I.
PROSITE, PS00578, RIBOSOMAL_S6E, 1.
  PRT;
  EMBL; AF154066; AAF04789.1; -.
InterPro; IPR001377; Ribosomal S6E.
  33.5%;
   Local Similarity 49.5
nes 45; Conservative
  STANDARD;
   STANDARD;
  Mycobacterium smegmatis.
  SEQUENCE FROM N.A.
   NCBI_TaxID=1772;
   DBH MYCSM
Q9ZHC5;
  HUP OR HLP
  Query Match
   DBH_MYCSM
AC DBH M
DT 16-0C
DT 16-0C
DT 16-0C
DE DNA-1
GSN MYCCD
OC BACT!
OC BACT!
OC ACTIN
CO ACTIN
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   4
  Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.;
"Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins.";
Infect. Immin. 59:3685-3693(1991).
--- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
Mol. Gen. Genet. 260:475-479(1998).
-!- PUNCTION: THIS PROTEIN BELCHOGS TO THE HISTONE LIKE FAMILY OF PROKENYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
  111 AKKAAKKAAPAKKAAAKTAATKAAAKKAPAKKAATKAPAKKAATKAPAKKAA 170
   Gaps
   1 AKKYAKK---EKAYAKK--AEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEK-- 51
   .,
6
   DB 1; Length 208;
  PROBLES, PS00045; HISTONE LIKE; 1.

DNA-binding; DNA condensation; Repeat.

DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN 101 205 DEGENERATE REPEATS REGION.
   33.4%; Score 136.5; DB 1; Length 51.6%; Pred. No. 0.0012; tive 6; Mismatches 29; Indels
  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB)
  CASF577F61F7EF09 CRC64;
  Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=162;
  -!- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
  384 AA
  52 KEYAAAEAKYKAEAAKKAYKAEAAKAAAKEA 82
  PRT;
  EMBL; AF068138; AAD13809.1; -.
HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac_DNAbind.
Pfam; PF00216; Bac_DNA_binding; 1.
Probom; PD000946; Bac_DNA_binding; 1.
SMART; SM00411; BHL; 1.
  MEDLINE=91372983; PubMed=1894368;
   208 AA; 21230 MW;
  Best Local Similarity 51.6
Matches 47; Conservative
  STANDARD;
  reponema phagedenis
   LARGE MOLECULES
  SEQUENCE FROM N.A.
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   3,
  1-10.
1-11.
1-12.
1-13.
1-15.
1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-A-A-B.
                                    TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
   5; Gaps
   1 AKKYAKKEKAYAKKA--EKAAKK--AEAKAYKAAEAKKKAKAEAKKYAKAAKAE-KKEYA 55
   ZUOI OR YGR28SC.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacese; Saccharomyces.
  Score 133.5; DB 1; Length 384;
Pred. No. 0.0032;
9; Mismatches 30; Indels 5;
  Zhang S., Lockshin C., Herbert A., Winter E., Rich A.;
"Zuotin, a putative Z-DNA binding protein in Saccharomyces
   6E94CBC74294DE8C CRC64;
   01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
  9; Mismatches
   433 AA
   SEQUENCE FROM N.A., AND SEQUENCE OF 1-10
   56 AAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
  PRT;
   STRAIN=20B-12;
MEDLINE=93010971; PubMed=1396572;
   ÉEQUENCE FROM N.A.
STRAIN-S288c / FY1679;
MEDLINE-97245295; PubMed-9090054;
                 Antigen; Outer membrane; Repeat;
   四
   42677 MW;
   32.6%;
   EMBO J. 11:3787-3796(1992)
       EMBL; M58563; AAA27480.1;
PIR; B43592; B43592.
  Query Match
Best Local Similarity 50.09
   STANDARD;
  243
252
261
270
  288
  384 AA;
  NCBI_TaxID=4932;
  ZUO1 YEAST
P32527;
   cerevisiae.
  SEQUENCE
  REPEAT
REPEAT
   DOMAIN
  REPEAT
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   ë,
Volckaert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including ZUO1, BGL2 and BIO2 genes and an ABC transporter gene.";
Yeast 13:251-259(1997).
-i- FUNCTION: Z-DNA BINING PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION.
   7; Сарв
   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKA-AKAEKKEYAAAEAK 60
  DB 1; Length 433;
   Indels
   J-DÖMAIN.
ALA/LYS-RICH.
, 0AA76BC11D3C7DAB CRC64;
   32.6%; Score 133.5; DB 1;
Local Similarity 47.6%; Pred. No. 0.0035;
Ne 40; Conservative 12; Mismatches 25;
   Fram; rroces, 2
SMART; SM00271; DnaJ; 1.
PROSITE; PS00036; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
Chaperone; DNA-binding; Nuclear protein.
  Search completed: March 10, 2003, 12:17:10 Job time : 19.5949 secs
  -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 J DOMAIN.
   345 EAAKAAKKKNK-RAIRNSAKEADY 367
  84
  433 AA; 49019 MW;
   EMBL; Z73070; CAA97317.1; -. PIR; S25194; S25194. HSSP; P08622; 1BQZ. SGD; S0003517; ZUO1. InterPro; IPR001623; DnaJ N. Pfam; PF00226; DnaJ; 1.
  61 YKAEAAKKAYKAEAAKAAAKEAAY
   EMBL; X63612; CAA45156.1; -. EMBL; Z73070; CAA97317.1; -.
  357
   SEQUENCE
  Query Match
   DOMAIN
   Matches
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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|                          |                         | (without alignments)<br>389.109 Million cell updates | updatee |
|--------------------------|-------------------------|------------------------------------------------------|---------|
| Title:<br>Perfect score: | US-09-816-989A-6<br>409 |                                                      |         |

Minimum DB seq length: 0 Maximum DB seq length: 200000000

| 80               | 100%    | 45 gummaries |
|------------------|---------|--------------|
| Match            | Match   | first        |
| Minimum          | Maximum | Listing      |
| Post-processing: |         |              |

| SPTREMBL 21:* | 1: sp_archea:* | 2: sp_bacteria:* | 4: sp_human:* | 5: sp_invertebrate:* | ds : | 7: sp_mhc:* | <br>de: | 10: sp_plant:* | :: | <br><pre>13: sp_vertebrate:*</pre> | 14: sp_unclassified:* | 15: sp_rvirus:* | <pre>16: sp_bacteriap:*</pre> | 17: sp_archeap:* |
|---------------|----------------|------------------|---------------|----------------------|------|-------------|---------|----------------|----|------------------------------------|-----------------------|-----------------|-------------------------------|------------------|
| Database :    |                |                  |               |                      |      |             |         |                |    |                                    | •                     |                 |                               |                  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Contract |   |        | Description            |     | Q82QT6 Q82QT6 salmonella | 99WWX1 Dseudomonas | •     |       |      | 0    |      | 9576 chlamydomon |      | Q8ZGZ2 yersinia pe | 0    | IXVN7 08xvn7 ralstonia s |       |       | Q90ZD7 Q90Zd7 bufo bufo q |   |
|----------|---|--------|------------------------|-----|--------------------------|--------------------|-------|-------|------|------|------|------------------|------|--------------------|------|--------------------------|-------|-------|---------------------------|---|
|          |   |        | £                      | ; ? | Š                        | 9                  | ŏ     | 061   | ŏ    | 6    | ö    | Ö                | Ö    | ŏ                  | 8    | ŏ                        | 056   | 6     | ö                         |   |
|          |   |        | DB                     | : ; | 9                        | N                  | 16    | S     | 19   | ~    | 16   | 10               | 16   | 16                 | ß    | 16                       | S     | m     | 13                        |   |
|          |   |        | Length                 |     | 407                      | 372                | 376   | 1701  | 394  | 395  | 1341 | 232              | 389  | 388                | 1866 | 200                      | 1128  | 212   | 224                       |   |
|          | ф | Query  | ore Match Length DB II |     | 40.0                     | 39.9               | 38.5  | 38.3  | 37.9 | 37.7 | 36.9 | 36.3             | 36.2 | 36.1               | 35.7 | 34.0                     | 33.6  | 32.9  | 32.2                      |   |
|          |   |        | Score                  |     | 165.5                    | 163                | 157.5 | 156.5 | 155  | 154  | 151  | 148.5            | 148  | 147.5              | 146  | 139                      | 137.5 | 134.5 | 131.5                     |   |
|          |   | Result | No.                    | 1 7 | -                        | 7                  | m     | 4     | S    | y    | 7    | œ                | σ    | 10                 | 11   | 12                       | 13    | 14    | 15                        | • |

| Q92a67 listeria in<br>O01395 drosophila<br>Q8rxdo arabidopsis | ysbuve arabiuopsis<br>Q9fp71 oryza sativ<br>O8t5c9 plasmodium |                  |                  | Q95s18 drosophila | O65794 triticum ae<br>O39598 chlamydomon | 065795 triticum ae | Q9y1p8 plasmodium | Q9ru45 deinococcus | O.     | Q9ndi9 plasmodium |        |        | Q9v6s7 drosophila | . 046142 mytilus edu | 0 vibrio | O46141 mytilus edu | 046362 mytilus edu |        |        | . Q9at22 lathyrus sa | Q9sxq8 pisum sativ |
|---------------------------------------------------------------|---------------------------------------------------------------|------------------|------------------|-------------------|------------------------------------------|--------------------|-------------------|--------------------|--------|-------------------|--------|--------|-------------------|----------------------|----------|--------------------|--------------------|--------|--------|----------------------|--------------------|
| Q92A67<br>O01395<br>Q8RXD0                                    | Q9FP71<br>Q9FP71<br>O8T5C9                                    | Q8WQ44<br>Q8T9R3 | Q9XHL9<br>084528 | 095818            | 065794<br>039598                         | 065795             | Q9Y1P8            | Q9RU45             | 60DS60 | 6IQN6Ö            | Q45370 | Q52088 | 789V6Q            | 046142               | Q9KR10   | 046141             | 046362             | Q9SWU2 | Q92R20 | Q9AT22               | 80XS60             |
| 10 10 10                                                      | 2 2 2                                                         | ហល               | 0 0              |                   | 9 9                                      |                    |                   |                    | 0      |                   | ~      | ~      | ស                 | ഗ                    | 16       | വ                  | ß                  | 2      | 2      | 10                   | 10                 |
| 243                                                           | 755<br>1671                                                   | 111              | 275              | 619               | 284<br>265                               | 288                | 845               | 581                | 606    | 696               | 182    | 298    | 607               | 191                  | 356      | 191                | 191                | 237    | 295    | 295                  | 297                |
| 31.9<br>31.9                                                  | 31.5                                                          | 31.2             | 31.2             | 31.2              | 30.9                                     | 30.8               | 30.8              | 30.6               | 30.4   | 30.4              | 30.3   | 30.3   | 30.3              | 30.2                 | 30.1     | 30.0               | 30.0               | 30.0   | 30.0   | 30.0                 | 30.0               |
| 130.5<br>130.5<br>129.5                                       | 129                                                           | 127.5            | 127.5            | 127.5             | 126.5                                    | 126                | 126               | $\sim$             | 124.5  | 124.5             | 124    | 124    | 124               | 123.5                | 123      | 122.5              | 122.5              | 122.5  | 122.5  | 122.5                | 122.5              |
| 118                                                           | 5 7 C                                                         | 23 24            | 25               | 27                | 7<br>7<br>8<br>7<br>8<br>8               | 30                 | 31                | 32                 | 33     | 34                | 35     | 36     | 37                | 38                   | 39       | 40                 | 41                 | 42     | 43     | 44                   | 45                 |

## ALIGNMENTS

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<sup>1</sup> AKKYAKKEKAYAKKAEKAAK......KKAYKAEAAKAAAKEAAYEA 86 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

<sup>671580</sup> segs, 206047115 residues Searched:

<sup>671580</sup> Total number of hits satisfying chosen parameters:

N

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Salmonella
  STRAIN=YM;
  Query Match
  Local
   061164;
   061164
   Matches
  Matches
  RESULT 4
061164
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   Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J., "The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
   12; Gaps
  1 AKKYAKKEKA--YAKKAE-KAAKKAEAKAYKAA--EAKKKAKAEAKKYA-----KAAKA 49
  MEDLINESS 56422022; PubMed=8824639; MEDLINESS 56422022; PubMed=8824639; Medriquez-Herva J.J., Ramos J.; Ramos J.; Rance J.; Rance J.; Rance J.; Rance J.; Raracterization 178:5836 an OptL null mutant of Pseudomonas putida."; J. Bacteriol. 178:5836-5840[1996]. EMBL; X74218; CAB50780.1; -(1966). Interpro; PRO0624; Histone_HI/HS. PRO0624; HISTONEHS. SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
  rola protein.
STR(073).
Salmbnella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
  ch . 39.9%; Score 163; DB 2; Length 372; 1 Similarity 53.1%; Pred. No. 3.5e-05; 52; Conservative 12; Mismatches 22; Indels
  Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                    Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
52 KEYAAAEAKYKAEA----AKKAYKAEAAKAAA---KEAAYEA 86
   Last sequence update)
Last annotation update)
   Last sequence update)
Last annotation update)
   50 EKKEYAAAEAKYK-AEAAKKAYKAEAAKAAAKEAAYEA 86
  372 AA
  376 AA
   Created)
   Created)
  PRT;
  PRT;
   ceil envelope.";
J. Bacteriol. 178:1699-1706(1996).
  MEDLINE=96198174; PubMed=8626299;
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01-MAR-2002 (TYEMBLTEL: 20,
01-MAR-2002 (TYEMBLTEL: 20,
01-JUN-2002 (TYEMBLTEL: 21,
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   01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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  Pseudomonas putida
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  SEQUENCE FROM N.A.
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  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
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   STRAIN=MT-2
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   O9WWX1
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099WMX
1009WMX
1009WMX
101-NN
DT 01-NN

   RESULT 3

0828C1

1D 0828

DT 01-M

DT 01-M

DD 10-J

DD 77K

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  Darkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterics serovar Typhi CT18.";
  Gaps
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  1 AKKYAKKEKAYA---KKAEKAAKKAEAKAYKAAEAKKKKAKA-----EAKKYAKAAK---- 48
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYA----KAAKAEKKEYA 55
  15;
   DB 16; Length 376;
  19;
   Length 1701;
  malaria
   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
   MEDINE-98115903; PubMed-9448114;

Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.

"A family of chimeric erythrocyte binding proteins of malar parasites."

Parasites."

Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).

EMBL; AF031886; AAC05366.1; -.

SEQUENCE 1701 AA; 199268 MW; EDABEZDEFD87CE8A CRC64;
  Indels
  17; Indels
   Complete proteome.
SEQUENCE 376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Brythrocyte binding protein.
  18;
   DB 5;
   49 AEKKEYAA--AEAKYKAEAAKKA---YKAEAAKAAAKE 81
  38.5%; Score 157.5; DB 1
54.8%; Pred. No. 9.3e-05;
ive 10; Mismatches 17
  ch 38.3%; Score 156.5; DB 5 Similarity 53.5%; Pred. No. 0.00048; 53; Conservative 9; Mismatches 18
  PRT; 1701 AA
  185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 217
   56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
   Nature 413:848-852(2001).
EMBL; AL627268; CAD05209.1; -.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
  51; Conservative
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Best Local Similarity
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  NCBI_TaxID=73239;
  SEQUENCE FROM N.A
NCBI_TaxID=601;
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01-NOV-1996
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   01-OCT-2001
01-OCT-2001
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   039576
  Q98KG7
  Matches
  28
   223
  RESULT 7
   RESULT 8
   039576
1D Q3
AC Q3
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   C STRAIN-0157.H7 (RIMD 0509952;

X MEDLINE=21156231; PubMed=11258796;

A Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Hayashi T. , Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han G. S. Shiba T., Hattori M., Shinagawa H.;

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

T "Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 811-22(2001).

REMBL; AR005552; AAG55075.1; -.

REMBL; AR00308; ANTIFREEZEI.

R PRINTS; PRO0308; ANTIFREEZEI.

W Complete proteome.

W Complete proteome.
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  167 AKKKABABAKAAABAQKKABAAAALKKKABAABAABBAABBARKKAABEKAAADKKAABKA 226
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  1 AKKYAKKEKAYA----KKAEKAA----KKAEAKAYKAAEAKKKAKAEA----KKYAKAA 47
  STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBI_TaxID=556;
   Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia
  16;
   Length 394;
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   Last sequence update)
Last annotation update)
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53.1%; Pred. No. 0.00015;
ive 6; Mismatches 23;
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   48 KAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
  394 AA
  395 AA
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Best Local Similarity
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  SEQUENCE FROM N.A
  NCBI_TaxID=83334;
   Tola protein.
  51;
   Q8X965
  Q937K4
RESULT 6
09377
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01-D)
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DT 01-D)
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1177 AEELRQQEEAARLKAEADAKAKAEAEAQAQAEAEAKAQAEAEAKAKADAEAKAEAEAKAK 1236
   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
  1 AKKYAK---KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEKKYAKAAKAEKKEYAAA 57
   AKKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYAKA-----AKAEKKEY 54
  Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
   ..
60
                                     genes.";
  Length 1341;
   Length 395;
  Mesorhizobium loti.";

DNA Res. 7:331-338[2000).

EMBL; AP002997; BAB46847.1; -.

Hypothetian protein; Complete proteome.

SEQUENCE 1341 AA; 138670 MW; 79C5D8149C969BC8 CRC64;
   21; Indels
Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "characterization of the Erwinia chrysanthemi tol.pal ge Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ297985; CAC82708.1;
  7885; CAC82708.1; -. 395 AA; 41601 MW; 3C0C1DC12E181013 CRC64;
   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll1482.
   Created)
Last sequence update)
Last annotation update)
   sequence update)
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52.2%; Pred. No. 0.00098;
tive 14; Mismatches 21;
  37.7%; Score 154; DB 2;
53.3%; Pred. No. 0.00018;
cive 13; Mismatches 18;
  PRT; 1341 AA.
   232 AA.
   EAKAKAAEAAKEKAAADAAKKAEAAAAKKAA 254
  EAKYK-AEAAKKAYKAEAAK----AAAKEAA 83
   1237 ADAEAKAKADAEAKA-KADADAKAAAEQQA 1265
   55 AAAEAKYKAEAAKKAYKAEA-AKAAAKEAA 83
   Rhizobium loti (Mesorhizobium loti).
  (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sec
   PRT;
   STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
  (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 20, I
   Best Local Similarity 52.2% Matches 47; Conservative
   49; Conservative
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MEDLINE=21470413; PubMed=11586360; Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C. F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
   1 AKKYAKKEKAYAKKAEKAAKKAEA--KAYKAAEAKKKAKAEAKKYA----KAAKAEKKEY 54
   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 0:0-0(2002).
EMBL, AY042083; AAL105081.1;
SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
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   35.7%; Score 146; DB 5; Length 1866; 50.0%; Pred. No. 0.0032; ive 10; Mismatches 28; Indels 1
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   81447B04B30A7E7C CRC64;
  215 EVAEKAAADAAEKKAAAADAEKKAAAAAKKVAAAAEAK
  54 ------YAAAEAKYKAEAAKK-AYKAEAAKAAAKEAA 83
                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
   Last sequence update)
Last annotation update)
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45.2%; Pred. No. 0.00054;
iive 9; Mismatches 21
   55 A-AAEAKYKAEAAKK---AYKAEAAKAAAKEAAYEA 86
   Tola colicin import membrane protein.
TOLA OR YPO1123.
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   EMBL, AJ414146; CAC89966.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
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   Nature 413:523-527 (2001)
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   Best Local Similarity
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  STRAIN=CO-92
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01-JUN-2002
   01-JUN-2002
   Query Match
   Yersinia
   Query Match
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   Maebl
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   Matches
  RESULT 11
Q8T5C8
   Matches
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   MEDLINE-5612086; PubMed-8590479;
Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R.
"The organization structure and regulatory elements of Chlamydomonas histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
EMBL; U16726; AAA98452.1; -.
HSSP; P02259; 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR001386; Linkerhist N.
Pfam; PP000331; Linkerhist N.
ProDom; PD000033; Linkerhist N.
SMART; SM00526; H15; 1.
   103 AKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKAEKKPKKEGEKKKAAKPAKPAKEK 162
   Gaps
  2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAA------EAKKKAKAKAEAKKYAKAKAE-- 50
  1 AKKYAKKEKAYAKKAEKAAKKAEA-----KAYKAAEAKKKAKAEAKKYAKAAKAEK 51
   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006136; AAK03052.1; -. HSSP; P19934; ITOL.
  37;
  22;
  Score 148.5; DB 10; Length 232;
Pred. No. 0.00028;
7; Mismatches 29; Indels 37;
  Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
  Length 389;
  36.2%; Score 148; DB 16; Length 36
47.2%; Pred. No. 0.0005;
ive 11; Mismatches 23; Indels
   51 -----KKEYAAAEAKYKAEAAK-----KAYKAEAAKAAAKEAAYEA 86
  24693 MW; 2D006AE44A8FA037 CRC64;
  389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
  Last sequence update)
Last annotation update)
   388 AA
  Created)
   PRT;
   MEDLINE=21145866; PubMed=11248100;
   InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
  36.3%;
  01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
  50; Conservative
  47; Conservative
  PRELIMINARY;
   PRELIMINARY;
  Pasteurella multocida
  Query Match
Best Local Similarity
  232 AA;
  Complete proteome. SEQUENCE 389 AA;
  Best Local Similarity
   SEQUENCE FROM N.A.
NCBI_TaxID=3055
  NCBI_TaxID=747;
  TOLA OR PM0968
   STRAIN=PM70;
   082GZ2:
  SEQUENCE
  Query Match
  Q9CM70
  Matches
  Matches
   RESULT 9
Q9CM70
   RESULT %0
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Q8ZGZ2 ID Q6

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CTA2p (Fragment).
  Histone H1.
  SEQUENCE
  093946
   Q90ZD7
   090ZD7
   RESULT 14
   RESULT 15
  093946
  Q90ZD7
   셤
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   S.
  MEDLINE=93165082; PubMed=8381919; Otsu K., Donelson J.E., Kirchhoff L.V.; Interruption of a Trypanoma cruzi gene encoding a protein containing 14-amino acid repeats by targeted insertion of the neomycin
   68 AKKAAPAKKAAVKKVAAKKAPAAKKAAVKKVAAKKAAPAKKAAVKKVAAKKAPAAKKAA 127
   Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
  1 AKKYAKKEKAYAKK--AEK--AAKKAEAK---AYKAAEAKKKA--KAEAKKYAKAAKAEK 51
   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arliguenave Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
   12;
  Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
   Length 200;
  34.0%; Score 139; DB 16; Length 20
52.6%; Pred. No. 0.0012;
.ive 5; Mismatches 28; Indels
  200 AA; 19279 MW; D3831B590510272D CRC64;
   01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  Created)
Last sequence update)
Last annotation update)
128 ККАРААК---КАРААККАААКРААКРААКРА
   PRT; 1128 AA.
  200 AA
   52 KEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 86
   phosphotransferase gene.";
Mol. Biochem. Parasitol. 57:317-330(1993)
EMBL; L04603; AAA96494.1; -.
   InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR001230; Prenyl_site.
  Created)
  PRT;
   EMBL; AL646071; CAD16500.1; -.
InterPro; IPR000104; Antifreeze_1.
InterPro; IPR003993; treacle.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01503; TREACLE.
   MEDLINE=21681879; PubMed=11823852;
  Probable histone H1 protein. RSC2793 OR RS00453.
  01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
  01-NOV-1996 (TrEMBLrel. 01,
  50; Conservative
  PRELIMINARY;
  PRELIMINARY;
   SEQUENCE FROM N.A. STRAIN=SYLVIO X-10;
  Complete proteome. SEQUENCE 200 AA;
  Query Match
Best Local Similarity
  SEQUENCE PROM N.A.
  NCBI_TaxID=305;
   STRAIN-GMI1000;
   R27-2 protein.
  01-MAR-2002
   Ralstonia
  026947
  Q8XVN7
   RESULT 12
OBXVNA
DD QBXVNA
AC QBXXVN
AC QBXXVN
AC QBXXVN
AC QBXXVN
AC DT 01-MP
DT 01-MP
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DT 01
  RESULT 13
10 226947
10 02694
AC 02694
DT 01-NO
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  Matches
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3;
   ij
  947 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 1003
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Bufo.
NCBI TaxID=30331;
  51 KEEEARKKREEEAKKKEEEAKKKAEEAKKKEEEAKKAEEAKKAE------EAKKVEEAA 103
  5; Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
  SECUENCE FROM N.A.

Kaiser B., Kunkel W., Saluz H.P., Munder T.;

"Identification of Candid albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

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NON TER I 1
   7; Gaps
   7 KEKAYAKKABKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA 66
   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
  Length 1128;
   SEQUENCE FROM N.A.

Kim H., Kim S.;

"Two Functional Toad Histone H2A Genes Contain Different Core
Promoters: the TATA Box or the Inr Element.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
  Query Match 32.9%; Score 134.5; DB.3; Length 212; Best Local Similarity 46.2%; Pred. No. 0.0028; Matches 37; Conservative 10; Mismatches 26; Indels 7
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PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
SEQUENCE 1128 AA; 119686 MW; 7997745D32B83656 CRC64;
   212 AA; 24231 MW; 10C2122E9554A387 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  Last sequence update)
Last annotation update)
  Query Match 33.6%; Score 137.5; DB 5; Best Local Similarity 48.9%; Pred. No. 0.0086; Matches 43; Conservative 11; Mismatches 29;
   Ź
  224 AA.
  1004 TKVAEAEKOKAAEATKVAEAEKOKAAEA 1031
   60 KYKAEAAK-KAYKAEAAKAAKEAAYEA 86
  Created)
   PRT;
   Bufo bufo gargarizans (Asian toad).
   EMBL; AF255740; AAK66966.1; -.
InterPro; IPR001386; Histone_H1/H5.
   104 KKAEEAKKAEEEARKKAETA 123
  86
  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
   67 KKAYKAEAAKAAAKEAAYEA
  Candida albicans (Yeast).
   PRELIMINARY;
  PRELIMINARY;
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Pfam; PF00538; linker histone; 1.
PRINTS; PR01574; TUBBYPROTEIN.
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   8 8 8
```

3, Query Match 32.2%; Score 131.5; DB 13; Length 224; Best Local Similarity 47.7%; Pred. No. 0.005; Matches 42; Conservative 9; Mismatches 28; Indels 9; Gaps

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Search completed: March 10, 2003, 12:25:58 Job time : 46.5401 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01; Search time 44.8143 Seconds (without alignments) 255.712 Million cell updates/sec Run on:

US-09-816-989A-6

score:

1 AKKYAKKEKAYAKKAEKAAK...........KAYKAEAAKAAAKEAAYEA 86 Sequence:

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908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

908470

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result |       | &<br>Query |                    |    |          |                    |
|--------|-------|------------|--------------------|----|----------|--------------------|
| No.    | Score | Match      | Match Length DB ID | DB | ai       | Description        |
| -      | 409   |            |                    | 21 | AAY82576 | Copolymer molecula |
| 8      | 351.5 |            |                    | 21 | AAY82575 | Copolymer molecula |
| m      | 312.5 |            | 109                | 21 | AAY82577 | Copolymer molecula |
| 4      | 268   |            |                    | 77 | AAY82574 | Copolymer molecula |
| S      | 233   |            |                    | 7  | AAY82573 | Copolymer molecula |
| 9      | 163   |            |                    | Ξ  | AAR06445 | Recombinant copoly |
| 7      | 157   |            |                    | Ξ  | AAR06446 | Recombinant copoly |
| 80     | 156   |            |                    | 21 | AAY98499 | Peptide #10 used i |
| 0      | 156   |            |                    | 7  | AAY59044 | Amino acid polymer |
| 10     | 156   | 38.1       |                    | 22 | AAU04289 | Poly-Lys-Ala used  |

| Nucleic acid trans M. tuberculosis hi | M. tuberculosis hi | Mycobacterium bovi | Trypanosoma cruzi |          | Trypanosoma cruzi | Synthetic helical | Zuotin. Saccharom | Human zuotin prote | S cerevisiae apopt | Amino acid sequenc | Quail H1 histone p | Plasmodium yoelii | Human histone H1 i | Human histone H1 i | Human histone H1 i | Copolymer molecula | Novel human diagno | Drosophila melanog | Peptide fragment o | Human linker histo |          |          |          | Human histone H1 i | Listeria monocytog | Neisseria meningit | Neisseria meningit | Histone H1-4, frag | Human linker histo | Adhesive polypepti | Human histone H1 i | Human histone H1 i | Human histone H1 i |
|---------------------------------------|--------------------|--------------------|-------------------|----------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAB45852<br>AAY34055                  | AAY57353           | AAB20575           | AAR84569          | AAR84565 | AAR84568          | AAR25206          | AAW30256          | AAY32954           | AAG70739           | AAY14928           | AAY76981           | AAB24128          | AAW29476           | AAY34033           | AAY57331           | AAY82572           | ABG28693           | ABB62173           | AAU09945           | AAE13237           | AAY34068 | AAY57366 | AAY34060 | AAY57358           | ABB49123           | AAY75540           | AAY75541           | AAU09944           | AAE13234           | AAW44829           | AAW29477           | AAY34034           | AAY57332           |
| 22                                    | 21                 | 21                 | 16                | 16       | 16                | 13                | 18                | 20                 | 22                 | 20                 | 21                 | 21                | 18                 | 20                 | 21                 | 21                 | 22                 | 22                 | 23                 | 23                 | 20       | 21       | 20       | 21                 | 23                 | 21                 | 21                 | 23                 | 23                 | 18                 | 18                 | 20                 | 21                 |
| 100                                   | 214                | 205                | 472               | 564      | 643               | 140               | 433               | 433                | 433                | 223                | 219                | 1507              | 222                | 222                | 222                | 45                 | 334                | 607                | 130                | 130                | 158      | 158      | 226      | 226                | 239                | 332                | 332                | 234                | 234                | 111                | 218                | 218                | 218                |
| 38.1                                  | 35.9               | 35.8               | ٠.                | 33.6     | 33.6              | 33.0              | 32.6              | ď.                 | 32.6               | ۲.                 |                    | Ή.                | 4                  | 급                  | 31.1               | ٥.                 | 30.3               | ٥.                 | 30.1               |                    | ę.       | 29.6     | 29.6     | 29.6               | ٥.                 | φ.                 | 6                  | 6                  | 6.                 | e,                 | 28.6               |                    | 28.6               |
| 156                                   | 147                |                    | 137.5             |          |                   | 135               |                   |                    | 133.5              | 129.5              | 129                | 127.5             | 127                | 127                | 127                | 126.5              | 124                | 124                | 123                | 123                | 121      | 121      | 121      | 121                | 121                |                    | 119.5              | _                  | 119                | 118.5              | 117                | 117                | 117                |
| 11                                    | 13                 | 14                 | 15                | 16       | 17                | 18                | 19                | 20                 | 21                 | 22                 | 23                 | 24                | 25                 | 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33       | 34       | 35       | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

AAY82576 standard; peptide; 86 AA 28-JUL-2000 (first entry) AAY82576; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

optopyment, morecuted metally marker, training the design of partitions Copolymer; molecular weight marker; TV-marker; immune disease; pemphigus vulgaris; systemic lupus erythematosus

Unidentified

WO200018794-A1

06-APR-2000

99WO-US22402. 24-SEP-1999;

98US-0101693. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

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셤
  AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune becompositis, autoimmune thyroiditis, autoimmune vecetinits, contact sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimoco's disease, idiopathic myxoedema, myasthenia gravis, permpias, pempiagus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-shost disease, and delayed-type hypersenaitivity. The polypeptides of the invention have defined molecular weights and phylacial properties which are analogous to allowed.
   ;
0
   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
   Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAAKAEKKEYAAAEAK 60
   ö
  100.0%; Score 409; DB 21; Length 86; 100.0%; Pred. No. 2.9e-30;
   Indels
   0; Mismatches
   61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
   AAY82575 standard; peptide; 77 AA
  Claim 10; Page 14; 72pp; English
   61 YKAEAAKKAYKAEAAKAAAKEAAYEA
  nolecular weight markers.
   86; Conservative
   WPI; 2000-317499/27.
   Similarity
  86 AA;
                   Lis D;
  Sequence
  Query Match
  Local
                   Gad A,
  Matches
   RESULT 2
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Sequence
   AAY82577;
  Query Match
  Matches
   RESULT 3
   AAY82577
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  셤
  Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinfiammatory antidiabetic; thyromimetic; haemoetatic; antipooriatic; dermatological; antidiamenory condition; multiple sclerosis; rheumatod arthritis; inflammatory condition; multiple sclerosis; rheumatod arthritis; diabetes mellitus; draves disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; draves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
  pemphigus vulgaris; systemic lupus erythematosus
   28-JUL-2000 (first entry)
   WO200018394-A1
   Unidentified
  AAY82575;
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셤 ò

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides [1) for determining the molecular invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of an an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune conditions, can active may be treated include either cell-mediated or antibody-mediated or solve diseases which may be treated include either cell-mediated or antibody-mediated architits, osteoarbritis, autoimmune haemolytic analemia, autoimmune oophoritis, osteoarbritis, autoimmune hemolytic analemia, autoimmune oophoritis, antoimmune thyroiditis, autoimmune cophoritis, osteoarbritis, autoimmune cophoritis, autoimmune solve and architis, osteoarbritis, autoimmune cophoritis, autoimmune cophoritis, autoimmune cophoritis, osteoarbritis, autoimmune cophoritis, osteoarbritis, autoimmune cophoritis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, osteoarbritis, disease, diabeten mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysoedema, mysathenia gravis, psorianis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which are invention have defined molecular weights and physical properties which are analogous to altionar and analogous properties which are analogous to altionar and analogous properties which are analogous to altionar and analogous properties whose and analogous to altionar and analogous properties and 
  glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopethic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemoatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.
   Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
  1 АККУАККЕКАУАККАЕКААККАЕАКАУКААЕАКККАКАБАККУАКААКАЕККЕУАААЕАК 60
   6
   glatiramer acetate molecules, which makes them ideal for use as
  Copolymer; molecular weight marker; TV-marker; immune disease;
  Score 351.5; DB 21; Length 77; Pred. No. 4.1e-25;
   0; Indels
   85.9%; Scor.
89.5%; Pred. No. *...
  61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  61 -----YKAEAAKAAAYEA 77
   AAY82577 standard; peptide; 109 AA
   Claim 10; Page 14; 72pp; English.
   CO LTD.
   98US-0101693.
   99WO-US22402.
  (YEDA ) YEDA RES & DEV CO LI
(TEVA-) TEVA PHARM USA INC.
   28-JUL-2000 (first entry)
  molecular weight markers.
  Local Similarity 89.5
les 77; Conservative
  WPI; 2000-317499/27.
   77 AA;
   24-SEP-1999;
   25-SEP-1998;
                            06-APR-2000.
   Gad A,
```

ij

(first entry)

28-JUL-2000

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inflammatory condition; multiple sclerosis; rheumatoid arthritis; cothi's disease; chronic immune thrombooyropaenia purpura; colitis; diabetes mellitus; graves disease; diallain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                     pemphigus vulgaris; systemic lupus erythematosus.
   Ą
  Claim 10; Page 14; 72pp; English.
  AAY82574 standard; peptide; 66
   (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
   76.48;
72.18;
  99WO-US22402.
  98US-0101693
  Best Local Similarry
Matches 80; Conservative
   molecular weight markers.
  WPI; 2000-317499/27.
  109 AA;
  WO200018794-A1
   Lis D;
  Unidentified
  24-SEP-1999;
  06-APR-2000
  Sequence
   AAY82574;
   Query Match
   Gad A,
  AAY82574
ID AAY8
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AC AAY8
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides markers for glatinamer acetate related tetrapolymers The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoric antoimmune beamolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune curectantis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gullain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lugus erythematosus. Mediated-mediated diseases which can be treated
   5
  t
C
AAY82571 to AAY82577 represent specifically claimed copolymer molecular
   include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensityity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
  Gaps
  1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA------36
   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAAKAKKE 60
  27;
   DB 21; Length 109;
   61 YKABAKKYAKAAKABKKEYAAABAK-KABAA-KAYKABAAKAAAKBAAYBA 109
  Indels
  37 - KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA
  3;
  Score 312.5; DB
Pred. No. 2e-21;
1; Mismatches
```

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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mallitus; Graves disease; Gulliain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
  AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or
  uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, crohact sensitivity disease, diabetes mellitus, Graves disease, duilain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
   include host-versus-graft disease, graft-versus-host disease, and delayde-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
   antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune cophoritis, autoimmune
   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
   20; Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAKAEKKEYAAAEAK 60
  1 AKKYAKKEKAYAK-----AKKAEAK------AAKKAKAEAKKYAKAKAKAEKEKEYAAAEAK 49
   65.5%; Score 268; DB 21; Length 66;
   Indels
  1.3e-17
   0; Mismatches
   Pred. No.
   Claim 10; Page 14; 72pp; English.
  61 YKAEAAKKAYKAEAAKAAAKEAAYEA
   (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
  99WO-US22402.
  98US-0101693.
  75.6%;
   Conservative
   WPI; 2000-317499/27.
  Local Similarity
  66 AA;
   WO200018794-A1.
  Gad A, Lis D;
  24-SEP-1999;
  25-SEP-1998;
   06-APR-2000
   65;
  Sequence
   Query Match
   Matches
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AAY82573 standard; peptide; 56 AA
  Claim 10; Page 14; 72pp; English
   LTD.
  99WO-US22402.
   98US-0101693.
  (YEDA ) YEDA RES & DEV CO L'
(TEVA-) TEVA PHARM USA INC.
                                 (first entry)
  molecular weight markers
   WPI; 2000-317499/27.
   Ź
   WO200018794-A1
  Gad A, Lis D;
   25-SEP-1998;
  24-SEP-1999;
                                28-JUL-2000
  06-APR-2000
  Sequence
                         AAY82573;
20
              RESULT 5
셤
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for and an amino acid composition are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune either cell-mediated or canediated diseases and inflammatory conditions, e.g. multiple campellinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinits, Crohn's disease, chornic immune thrombocytopaenia purpura, colltis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimcto's disease, and inpartic myxoedema, myasthenia gravis, permoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to molecular weights molecules, which makes them ideal for use as
Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
```

57.0%; Score 233; DB 21; Length 56;

Query Match 🗸

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90US-0473845.
89US-0312541.
   90EP-0301700
   (first entry)
          54; Conservative
   (REPL-) REPLIGEN CORP
  WPI; 1990-255848/34.
N-PSDB; AAQ05664.
Best Local Similarity
  154 AA;
  See also AAQ05665
  16-FEB-1990;
   17-FEB-1989;
   03-JAN-1991
  07-FEB-1990;
   22-AUG-1990
  EP383620-A.
   Synthetic
   AAR06445;
  Sequence
   Cook KS;
   certain
          Matches
   AAR06445
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  Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinfiammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidamento; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
-----YKAEAAKAAAKEAAYEA 66
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US469100), NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences, originaling from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein.

C COP-1-77 contains oligonucleotide duplexes incoding the following sequents: YKK, BER, KAK, ARA, and AAA. The N-terminal annine residue is left behind following C arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to conter beneficial effects on damaged hair or as supplements for diets deficient in
  7;
  30; Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAEAKKKAKAKAEAKKYAKAAAKAEKKEYAAAEAK 60
   Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
   Score 163; DB 11; Length 154; Pred. No. 1e-07;
  Producing genes encoding random polymers of aminoacid(s) - 3 producing recombinant polypeptide(s) with biological and/or immunological activity
   Recombinant copolymer 1-77, myelin basic protein analogue.
  Indels
62.8%; Pred. No. 1.6e-14;
ive 2; Mismatches 0;
  1 АККҮАККЕКАУАККАЕКААККАЕАКАУКААЕАКККАЕАК----
  AAR06445 standard; protein; 154 AA
   61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  40 -----YKAEAAKAAKEAYEA 56
   Disclosure; Fig 11; 25pp; English.
  39.9%;
42.3%;
  Query Match
Best Local Similarity
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5;

Length 106;

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Query Match
Best Local Similarity
      106 AA;
  100 AA;
   14-DEC-1993;
   20-MAR-1992;
  19-MAR-1993;
  degradation.
   US6033884-A.
  07-MAR-2000.
   51;
  Synthetic.
      Sequence
   AAY98499;
  Sequence
  Query Match
   Matches
  RESULT 8
AAY98499
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  To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1.99 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, EKA, RKA, REA, AAR KEA, and AAA. The Neterminal alanine residue is left behind following CNBr cleavage of the
  Gaps
                                     41 ---KKYAKAAKAEKKEYAAAEAKYKAEA--------AKKAYKAEAAKAA-- 78
   The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids.
       46;
                          2 KKYAK--KEKAYAKKAEKA--AKKAEAKAY-KAAEAKKKAKAEA------
   Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunologicál activity; autoimmune encephalomyelitis; multiple sclerosis;
  Producing genes encoding random polymers of aminoacid(s) - 5 producing recombinant polypeptide(s) with biological and/or immunological activity
  Recombinant copolymer 1-19, myelin basic protein analogue.
       Indels
      20;
     9; Mismatches
  AAR06446 standard; protein; 106 AA.
  Disclosure; Fig 12; 25pp; English.
  90US-0473845.
89US-0312541.
   90EP-0301700
   (first entry)
     55; Conservative
  (REPL-) REPLIGEN CORP
   WPI; 1990-255848/34.
   132 AEKAKEAEYK 141
  79 ---AKEAAYE 85
  N-PSDB; AAQ06446
  fusion protein.
  16-FEB-1990;
  07-FEB-1990;
17-FEB-1989;
   03-JAN-1991
  22-AUG-1990.
   EP383620-A.
  Synthetic
  AAR06446;
   Cook KS;
Matches
  RESULT 7
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA3663-A36652 and peptide sequences AAA98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver once the acids to hepatocytes, muscle cells or bone forming cells, e.g. transporter systems are also used to create transgenic animals (as models for transporter systems are also used to create transgenic animals (as models for thuman carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
  System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
  Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEK-----KE 53
   Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
  12;
  38.1%; Score 156; DB 21; Length 100;
  Smith LC;
  20; Indels
  Peptide #10 used in nucleic acid transporter system.
  WOO SLC,
Score 157; DB 11;
Pred. No. 2.4e-07;
9; Mismatches 20;
   Disclosure; Column 125-128; 108pp; English
  54 YAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
  Gottchalk S, Sparrow J, Cristiano RJ,
  ¥.
  AAY98499 standard; Peptide; 100
  (BAYU ) BAYLOR COLLEGE MEDICINE.
    38.4%;
55.4%;
  93US-0167641.
  93WO-US02725.
   92US-0855389.
  31-JUL-2000 (first entry)
  Conservative
  WPI; 2000-281993/24.
```

Gaps

5;

Indels

30;

6; Mismatches

47; Conservative

Matches

Length 100;

Score 156; DB 21; Pred. No. 2.7e-07;

38.1%; 55.3%;

Query Match Best Local Similarity

100 AA;

Sequence

X S

1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58

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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognises and binds to a cell surface receptor or artigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through cytosis; (c) a nucleic cor (e) a lysis moiety that enables the transport of the entire complex or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS calls of specific acid into the cellular interior as well as the nucleus of specific acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an immal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The Acid are acid as agent within the NTS avoids the problem of endosomal/lysosomal
                      7
   /note= "Lys-Ala in positions 3 to 100 may be optionally
   Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                     Gaps
  1 AKKYAK-KEKAYAKKAEKAAKKAEAXAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
  cytosis;
   Nucleic acid transport system; NTS; cell surface receptor; cytosi
nuclear membrane; lysis moiety; transgenic animal; human disease;
nucleic acid delivery; cancer.
                     5
  Smith LC;
                     30; Indels
  Sparrow J,
   Pred. No. 2.7e-07;
6; Mismatches 30
   Amino acid polymer seq ID NO: 64 of US5994109
   Disclosure; Columns 123-124; 107pp; English.
  Gottchalk S,
   Location/Qualifiers
  AAY59044 standard; peptide; 100 AA
  59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
   COLLEGE MEDICINE.
   absent "
  93US-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
 55.3%;
  95US-0460890.
   (first entry)
                   47; Conservative
  Cristiano RJ,
Best Local Similarity
Matches 47; Conserv
   WPI; 2000-038262/03
  Misc-difference 3
  (BAYU ) BAYLOR
   07-MAR-2000
  03-JUN-1995;
   14-DEC-1993;
   20-MAR-1992;
19-MAR-1993;
  US5994109-A
   degradat kon
  30-NOV-1999
   14-DEC-1993
  Synthetic
  AAY59044;
  WOO SLC,
   62
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  The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
  Nucleic acid transport, cytosis; ligand, lysis agent; spacer molecule; gene therapy, hepatocyte; muscle; bone forming cell.
  animals
   Gaps
/note= "Lys-Ala in positions 3-100 may be present or absent"
   5;
   Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
   <u>ب</u>
  Length 100;
  Sparrow
   Indels
   Poly-Lys-Ala used in nucleic acid transporter system.
   30,
  ŝ
   ch 38.1%; Score 156; DB 22; 1 Similarity 55.3%; Pred. No. 2.7e-07; 47; Conservative 6; Mismatches 30;
  Gottchalk
  Disclosure, Column 131, 111pp; English
  Location/Qualifiers 3..100
  AAU04289 standard; Peptide; 100 AA
   Cristiano RJ,
  83
  86
   BAYU ) BAYLOR COLLEGE MEDICINE
  59 AKYKAEAAKKAYKAEAAKAAAKEAA
  62 AKAKAKAKAKAKAKAKAKAKA
   92US-0855389.
  95US-0462040
  93US-0167641
   (first entry)
   Smith LC,
  WPI; 2001-365933/38
   Query Match
Best Local Similarity
Matches 47; Conserv
   100 AA;
   Misc-difference
   Nucleic acid
   US6177554-B1
  05-JUN-1995;
   14-DEC-1993;
  19-MAR-1993;
   23-OCT-2001
  23-JAN-2001.
  0-MAR-1992
   Synthetic
   AAU04289;
   WOO SLC,
   Sequence
  10
   RESULT 10
AAU04289
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|| ||:| || || AKAKAKAKAKAKAKA 86

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Ulcerative colitis; histone; H1-like antigen; porin antigen;
Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis;
perinuclear anti-neutrophil cytoplasmic antibody.
  M. tuberculosis histone H1-like antigen.
   AAY34055 standard; protein; 214 AA
  59 AKYKAEAAKKAYKAEAAKAAAKEAA
  Mycobacterium tuberculosis.
   23-NOV-1999 (first entry)
  WO9945955-A1
  16-SEP-1999.
   AAY34055;
  62
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   This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding to a cell, comprising a binding complex comprising a ligand binding conclete acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a cuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, such as hormones, growth factors, enzymes, clotting factors, suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
   growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
  Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
   Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                      1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE
  38.1%; Score 156; DB 22; Length 100; 55.3%; Pred. No. 2.7e-07; ive 6; Mismatches 30; Indels
  Nucleic acid transporter system peptide ligand SEQ ID NO 64.
   WOO SLC;
   Smith LC,
   Disclosure; Column 125-126; 105pp; English.
   Cristiano RJ,
   AAB45852 standard; Protein; 100 AA
  83
   86
   (BAYU ) BAYLOR COLLEGE MEDICINE
   || ||:| || || AKAKAKAKAKAKAKA
  59 AKYKAEAAKKAYKAEAAKAAAKEAA
  93US-0167641.
  95US-0460971
   92US-0855389.
  (first entry)
   Ouery Match
Best Local Similarity 55.3'
  Gottchalk S, Sparrow J,
  WPI; 2001-049093/06.
  100 AA;
   Unidentified.
  05-JUN-1995;
   14-DEC-1993;
  19-MAR-1993;
  21-MAR-2001
   US6150168-A.
   21-NOV-2000.
   20-MAR-1992
  AAB45852;
   Sequence
  62
  AAB45852

AAB45852

AAB47

AAB
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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a control antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (DANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the pANCA-reacting the presence or absence of the complex, where the presence of the complex; indicates that the subject has UC. The pANCA-reactive histone H1-like antigen are useful in the antigen, porin antigen and Bacteroides antigen are useful in the diagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence represents a M. tuberculosis histone H1-like antigen.
  111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
   34; Indels 10; Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
  Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
  35.9%; Score 147; DB 20; Length 214; 50.0%; Pred. No. 4.1e-06; tive 3; Mismatches 34; Indels 10
   169 TKAVKKTAVKASVRKAATKAPAKKAAKRPATKA 202
   55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  Claim 2; Fig 11; 134pp; English.
   98US-0041889.
99WO-US05492
   Local Similarity 50.03
nes 47; Conservative
  (REGC ) UNIV CALIFORNIA.
   WPI; 1999-551215/46.
   Braun J, Cohavy O;
   214 AA;
12-MAR-1999;
   12-MAR-1998;
   Sequence
  Query Match
   Matches
   8
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3;

Gaps

1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58

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(first entry)
   Conservative
  OTSUKA PHARM CO
YAMADA T.
   ŝ
   such as tuberculosis
   Yamada T, Matsumoto
  (SAKA ) OTSUKA PHARM (YAMA/) YAMADA T. (MATS/) MATSUMOTO S.
                               Mycobacterium bovis
  WPI; 2000-543393/49.
  Local Similarity
   205 AA;
   Trypanosoma cruzi.
  N-PSDB; AAA88001
  WO200044905-A1
  29-JAN-1999;
  WO9525797-A1
  03-AUG-2000.
  09-MAY-1996
   48;
   28-SEP-1995
   AAR84569;
  Sequence
   Query Match
  Key
Region
  Best Loc
Matches
   09
   RESULT 15
   AAR84569
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   The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. The present sequence represents a histone H1-like protein of M. tuberculosis, designated 214.
   Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
  111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
   Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb;
pANCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein;
   Gaps
   Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1; MDP1; slcw growing acid-fast bacterium protein; immunogenicity;
  1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
  Score 147; DB 21; Length 214;
Pred. No. 4.1e-06;
3; Mismatches 34; Indels 10;
  Mydobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
   M. tuberculosis histone H1-like protein, 214.
   169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
   86
  55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA
                     AAY57353 standard; Protein; 214 AA
  ¥.
   Example 5; Fig 10; 49pp; English
   AAB20575 standard; Protein; 205
   35.9%;
   98US-0041889
  96US-0057846
   97US-0837058
   Mycobacterium tuberculosis.
  (first entry)
  (first entry)
  47; Conservative
  (REGC ) UNIV CALIFORNIA.
  histone H1; isoform.
   Query Match
Best Local Similarity
   WPI; 2000-255695/22.
   Braun J;
   214 AA;
   12-MAR-1998;
   12-APR-1996;
  13-JUN-2000
  11-APR-1997;
   08-DEC-2000
  US6033864-A
  07-MAR-2000
   Cohavy 0,
  AAY57353;
   Sequence
   AAB20575;
   Matches
RESULT 13
           AAY57353
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The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used for diagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
   New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
  111 AKKVAK--KAPAKKATKAAKKAATK----APAKKAATKAPAKKAVKATKSPAKKVTKAVK 164
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKA-KAEAKKYAKAAKAEKKEYAAAEA 59
   241..450
/label= repeat_region
/note= "15 of 69 repeat units of 14 amino acids"
   TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
  6
  DB 21; Length 205;
pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC;
Mycobacterium avium intracellular complex; Hansen's disease.
  35.8%; Score 146.5; DB 21; 53.9%; Pred. No. 4.3e-06; tive 3; Mismatches 29;
   Trypanosoma cruzi TCR27 polypeptide, Ag8.
  165 KTAVKASVRKAATKAPAKKAAAKRPATKA 193
  86
  Location/Qualifiers
  K--YKAEAAKKAYKAEAAKAAAKEAAYEA
   AAR84569 standard; Protein; 472 AA
   Claim 1; Fig 2A; 62pp; Japanese.
   99JP-0022588.
   28-JAN-2000; 2000WO-JP00455.
```

Query Match 33.6%; Score 137.5; DB 16; Length 472; Best Local Similarity 48.9%; Pred. No. 6.9e-05; Matches 43; Conservative 11; Mismatches 29; Indels 5; Gaps

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60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86

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Search completed: March 10, 2003, 12:21:30 Job time : 44.8143 secs

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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-816-989A-6

score:

1 AKKYAKKEKAYAKKAEKAAK.......KKAYKAEAAKAAAKEAAYEA Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188354 segs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database :

//cgn2 //cgnata///pubpaa/US09 PUBCOMB.pep:#
/cgn2 6/ptodata///pubpaa/US10 NEW PUB.pep:#
/cgn2 6/ptodata///pubpaa/US10 NEW PUB.pep:#
/cgn2 6/ptodata///pubpaa/US10 PUBCOMB.pep:#
/cgn2 6/ptodata///pubpaa/US60 NEW PUB.pep:#
/cgn2 6/ptodata///pubpaa/US60 NEW PUB.pep:#
/cgn2 6/ptodata///pubpaa/US60 NEW PUB.pep:# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Description    | Sequence 6, Appli                 | Ŋ                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 4                                                                                                                                                                                                                              | Sequence 3, Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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| DB             | 101                               | 10                                                                                                                                | 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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| Length         | 98                                | 77                                                                                                                                | 109                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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| Query<br>Match | 100.0                             | 85.9                                                                                                                              | 76.4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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Sequence 3</td></t<> | Score Match Length DB ID Description  409 100.0 86 10 US-09-816-989A-5 Sequence 6, 312.5 85.9 77 10 US-09-816-989A-5 Sequence 5, 312.5 76.4 109 10 US-09-816-989A-7 Sequence 7, 268 65.5 66 10 US-09-816-989A-7 Sequence 7, 27 10 US-09-820-81A-8 Sequence 2, 129.5 31.7 223 9 US-10-184-832-5 Sequence 2, 129.5 31.7 223 9 US-10-184-832-5 Sequence 2, 129.5 31.7 223 9 US-10-184-832-5 Sequence 2, 129.5 31.7 223 9 US-09-820-843A-24 Sequence 2, 110.5 27.0 57 10 US-09-820-843A-24 Sequence 2, 110.5 27.0 57 10 US-09-820-843A-23 Sequence 2, 110.5 27.0 57 10 US-09-821-80A-3 Sequence 3, 110.5 27.0 57 10 US-09-821-80A-3 Sequence 5, 500.8 56.5 500 9 US-09-738-526-5197 Sequence 5, 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500.8 56.5 500. | Score Match Length DB ID Description  409 100.0 86 10 US-09-816-989A-6 Sequence 6 312.5 85.9 77 10 US-09-816-989A-5 Sequence 5 312.5 86.9 77 10 US-09-816-989A-7 Sequence 7 233 57.0 56 10 US-09-816-989A-3 Sequence 7 131 32.0 45.9 US-09-816-989A-3 Sequence 8, 131 32.0 45.9 US-09-816-989A-3 Sequence 20, 129.5 31.7 223 9 US-09-816-989A-2 Sequence 20, 129.5 31.7 223 9 US-09-816-989A-2 Sequence 20, 126.5 80 US-09-816-989A-2 Sequence 21, 129.5 31.7 223 9 US-09-816-989A-2 Sequence 21, 125.5 30.9 US-09-816-989A-2 Sequence 24, 112.5 27.5 36.9 US-09-820-843A-24 Sequence 24, 110.5 27.0 617 10 US-09-820-843A-95 Sequence 31, 100.5 27.0 617 10 US-09-864-761-36182 Sequence 31, 100.5 27.0 617 10 US-09-864-761-36182 Sequence 21, 100.5 26.4 35 10 US-09-816-989A-1 Sequence 51, 100.8 26.4 36.4 36.8 26.8 36.8 36.8 36.8 36.8 36.8 36.8 | Query         Query           409         100.0         86         10         US-09-816-989A-6         Sequence 6           351.5         85.9         77         10         US-09-816-989A-5         Sequence 5           351.5         85.9         77         10         US-09-816-989A-7         Sequence 5           312.5         56.10         US-09-816-989A-7         Sequence 7         Sequence 3           33         57.0         56         10         US-09-816-989A-3         Sequence 3           142         34.7         372         9         US-09-816-989A-3         Sequence 3           133         57.0         56         10         US-09-816-989A-3         Sequence 3           131         32.0         45         9         US-09-816-989A-3         Sequence 2           129.5         31.7         223         9         US-09-816-989A-3         Sequence 2           126.5         30.9         45         10         US-09-820-843A-2         Sequence 2           126.5         30.1         356         9         US-09-820-843A-2         Sequence 3           110.5         27.5         369         9         US-09-820-843A-2         Sequence 3 |

| Sequence 13765, A   | Seguence 5298, Ap  | Sequence 12294, A   | Sequence 1, Appli | Sequence 46, Appl | Sequence 48, Appl | Sequence 90, Appl | Sequence 11216, A   | Sequence 5198, Ap  | Sequence 1164, Ap  | Sequence 38, Appl | Sequence 37061, A   | Sequence 5, Appli | Sequence 2, Appli | Sequence 559, App | Sequence 8, Appli | Sequence 8, Appli | Sequence 9, Appli | Sequence 5759, Ap  | Sequence 12408, A   | Sequence 5854, Ap  | Seguence 7, Appli | Sequence 53, Appl | Sequence 51, Appl | Sequence 69, Appl | Sequence 229, App  |
|---------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|---------------------|--------------------|--------------------|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|
| US-09-815-242-13765 | US-09-815-242-5298 | US-09-815-242-12294 | US-09-882-774-1   | US-09-999-724-46  | US-09-999-724-48  | US-09-999-724-90  | US-09-815-242-11216 | US-09-815-242-5198 | US-09-925-300-1164 | US-09-765-272-38  | US-09-864-761-37061 | US-10-093-892-5   | US-09-923-304-2   | US-09-925-302-559 | US-09-985-442-8   | US-09-983-580-8   | US-10-093-892-9   | US-09-815-242-5759 | US-09-815-242-12408 | US-09-738-626-5854 | US-09-820-843A-7  | US-09-883-825-53  | US-09-883-825-51  | US-09-971-536-69  | US-10-002-344A-229 |
| 10                  | 10                 | 70                  | σ                 | 0                 | σ                 | σ                 | 10                  | 10                 | 10                 | 10                | 10                  | σ                 | 10                | 10                | 0                 | 10                | σ                 | 10                 | 10                  | σ                  | σ                 | 10                | 10                | σ                 | σ                  |
| 892                 | 454                | 454                 | 619               | 118               | 218               | 102               | 829                 | 840                | 300                | 453               | 71                  | 105               | 220               | 265               | 84                | 84                | 96                | 318                | 318                 | 365                | 203               | 564               | 634               | 1463              | 16                 |
| 26.2                | 25.6               | 25.6                | 25.4              | 25.2              | 25.2              | 24.9              | 24.3                | 24.3               | 23.2               | 23.1              | 22.9                | 22.4              | 22.2              | 22.2              | 22.0              | 22.0              | 22.0              | 22.0               | 22.0                | 22.0               | 21.8              | 21.5              | 21.5              | 21.4              | 21.3               |
| 107                 | 104.5              | 104.5               | 104               | 103               | 103               | 102               | 99.5                | 99.5               | 95                 | 94.5              | 93.5                | 91.5              | 91                | 91                | 90                | 06                | 90                | 90                 | 90                  | 90                 | 89                | 88                | 88                | 87.5              | 87                 |
| 20                  | 21                 | 22                  | 23                | 24                | 25                | 26                | 27                  | 28                 | 29                 | 30                | 31                  | 32                | 33                | 34                | 35                | 36                | 37                | 38                 | 39                  | 40                 | 41                | 42                | 43                | 44                | 45                 |

### ALIGNMENTS

```
Sequence 6, Application US/09816989A

| Sequence 6, Application US/09816989A
| Patent No. US20020115103A1
| GENERAL INFORMATION:
| APPLICANT: Lis, Doris
| TITLE OF INVENTION: COOLUMER I RELATED POLYREPTIDES FOR USE AS MOLECULAR WEIGHT MARK!
| TITLE OF INVENTION: OND UNDER: US/09/816,989A
| TITLE OF INVENTION UNDER: US/09/816,989A
| CURRENT FILING DATE: 2001-03-23
| PRIOR PILING DATE: 1998-09-25
| PRIOR FILING DATE: 1998-09-24
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 6
| LENGTH: 86
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   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
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   Length 86;
  Indels
  100.0%; Score 409; DB 10;
ilarity 100.0%; Pred. No. 2.5e-28;
Conservative 0; Mismatches 0;
  TYPE: PRT ORGANISM: Artificial Sequence
   Query Match
Best Local Similarity
Matches 86; Conserv
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEKKYAKAEKKEYAAAEAK 60

61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86

61 YKAEAAKKAYKAEAAKAAAKEAAYEA

В

유 ð RESULT 2 US-09-816-989A-5 ; Sequence 5, Application US/09816989A

US20020115103A1

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APPLICANT: Lis, Doris
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
  APPLICANT: Lis, DOTAS
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
FILE OF INVENTION: WAS 1001-03-23
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
WUMBER OF SEQ ID NOS: 7
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  ij
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   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
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  20; Gaps
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  Length 56;
   Length 66
   Indels
  ..
0
   ch 57.0%; Score 233; DB 10;
1 Similarity 62.8%; Pred. No. 9e-14;
54; Conservative 2; Mismatches 0;
  Query Match 65.5%; Score 268; DB 10; Best Local Similarity 75.6%; Pred. No. 1.2e-16; Matches 65; Conservative 0; Mismatches 1;
  61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
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   Sequence 4, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
  Sequence 3, Application US/09816989A
Patent No. US20020111103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
  TYPE: PRT
ORGANISM: Artificial Sequence
  SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
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ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity
   RESULT 5
US-09-816-989A-3
                               RESULT 4
US-09-816-989A-4
   LENGTH: 66
   Best Loca
Matches
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  Sequence 7, Application US/09816989A

| Sequence 7, Application US/09816989A
| Patent No. US20020115103A1
| GENERAL INFORMATION:
| APPLICANT: Gad, Alexander
| APPLICANT: Lis, Doris
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| FILE REFERENCE: 2609/60807-A-PCT-US
| CURRENT FILING DATE: 2001-03-23
| PRIOR APPLICATION NUMBER: E0/101,693
| PRIOR PILING DATE: 1998-09-25
| PRIOR PILING DATE: 1999-09-24
| WUMBER OF SEQ ID NOS: 7
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 7.
GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT PELLING DATE: 1909/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO S: 7

LENGTH: 77
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  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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  9
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   DB 10; Length 77;
  61 YKABAKKYAKAKAEKKEYAAABAK-KAEAA-KAYKABAAKAAAKBAYBA 109
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  86
   -----YKAEAAKAAAKEAAYEA 77
   61 YKAEAAKKAYKAEAAKAAAKEAAYEA
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ORGANISM: Artificial Sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity
   Query Match
Best Local Similarity
  RESULT 3
US-09-816-989A-7
  LENGTH: 109
  FEATURE:
   Matches
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO. 2
   APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

APPLICANT: Tan, Paul L. J.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: Of System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008c2

CURRENT PAPLICATION NUMBER: USO9/156,181

PRIOR PILING DATE: 1998-09-17

PRIOR PILING DATE: 1998-09-17

PRIOR PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 208

SEQ ID NO 201

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
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  Sequence 2, Application US/09816989A
Patent No. US20020115103A1
GENERAL INPORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
   ORGANISM: Mycobacterium vaccae US-10-051-643-201
  TYPE: PRT
ORGANISM: Artificial Sequence
  153 KAEAKAEAKAEAKE 166
     68 KAYKAEAAKAAAKE 81
   US-09-816-989A-2
  TYPE: PRT
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   Sequence 8, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
  Sequence 5, Application US/10184832

Sequence 5, Application US/10184832

Publication No. US20030022857A1

GENERAL INFORMATION:

APPLICANT: Xu et al.

TITLE OF INVENTION: COMPOSITIONS AND WEIGHT DISORDERS, INCLUDING OBESITY

FILE REFERENCE: MPI2001-056PINM

CURRENT APPLICATION NUMBER: US/10/184,832

CURRENT FILING DATE: 2002-06-28

PRIOR FILING DATE: 2001-07-05

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

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  32.0%; Score 131; DB 9; Length 452; larity 52.7%; Pred. No. 0.00028; Conservative 8; Mismatches 23; Indels
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   61 YKAEAAKKAYKAEAAKAAAKEAAYEA
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   US-10-184-832-5
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  Query Match
  Local
   FEATURE:
   Best Loca
Matches
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Sequence 95, Application US/09820843A
Publication No. US20030039953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Council Of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 95
  % Sequence 23, Application US/09820843A

Sequence 23, Application US/09953A1

Publication No. US20030039963A1

Publication No. US2003003963A1

APPLICANT: Council of Scientific and Industrial Research

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
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US-09-820-8430-843-23
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) NAME/KEY: misc_feature

) OTHER INFORMATION: gi|3322751

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  55 AAAEAKYKAE-AAKKAYKAEAAK-----AAAKEAA 83
   FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
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   66 ----AKKAYKAEAAKAAAKEAAYEA 86
  ORGANISM: Pseudomonas aeruginosa
   LENGTH: 369
TYPE: PRT
ORGANISM: T. pallidum
   Query Match
Best Local Similarity
  RESULT 12
US-09-820-843A-95
   FEATURE:
   LENGTH:
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   APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPREBUCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
  TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEITILE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
THE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
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  Score 116; DB 9; Length 309;
Pred. No. 0.0034;
1; Mismatches 35; Indels 14; Gaps
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  ) NAME/KEY: misc_feature

) OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF

; NAME/KEY: misc_feature

) OTHER INFORMATION: gi|9951352

US-09-820-843A-24
  30.1%; Score 123; DB 9; Length 356;
42.6%; Pred. No. 0.001;
tive 13; Mismatches 27; Indels
   191 AKREKEVAAKAEQERLAKEKAAKEAADKAKKEKERAAKAEAERKAQEA 238
   47 AKAEKKEYAAAE----AKYKA--EAAKKAYKAE--AAKAAAKEAAYEA 86
  1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE
  Sequence 27, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
   US-09-820-843A-24
; Sequence 24, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
  61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
  NAME/KEY: misc feature
OTHER INFORMATION: tola protein
NAME/KEY: misc feature
OTHER INFORMATION: g1|955354
  ch 28.4%;
l Similarity 47.9%;
qui Conservative 1
  Best Local Similarity 42.6%
Matches 46; Conservative
   ORGANISM: Vibrio cholerae
   Best Local Similarity
Matches 4g; Conserv
   RESULT 10
US-09-820-843A-27
  US-09-820-843A-27
   TYPE: PRT
  Query Match
  Query Match
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  LENGTH:
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Patent No. US20020034520A1
GENERAL INFORMATION:
APPLICANT: POITO, Massimo
TITLE OF INVENTION: NEGATIVE BACTERIAL INFECTIONS AND ENDOTOXIN RELATED DISEASES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan
STREET: 1185 Avenue of the Americas
  ö
   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAKY 61
   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKY 61
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  DB 10; Length 617;
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
INFORMATION: EXPRESSED IN BARIN. SIGNAL = 5.6
INFORMATION: SWISSPROT HIT: P12036, EVALUE 2.00e-33
INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
  DB 10; Length 434;
  Indels
  Diskette, 3.50 inch, 1.44 Mb storage
  Query Match 27.0%; Score 110.5; DB 10; Best Local Similarity 39.0%; Pred. No. 0.021; Matches 32; Conservative 10; Mismatches 39;
   26.7%; Score 109; DB 10; 36.2%; Pred. No. 0.019; tive 11; Mismatches 40;
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COSTIGAT, James V.
REGISTRATION NUMBER: 576-008
REFERENCE/DOCKET NUMBER: 576-108
TELECOMMUNICATION INFORMATION:
TELEFRAME: (212) 302-8999
   COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
CONTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,280A
FILING DATE: July 29,1998
   306 KSPVKEEAKSPEKAKSPVKEEA 327
  62 KAEAAKKAYKAEAAKAAAKEAA 83
  361 KKKKKKKKKKKKKKK 380
   62 KAEAAKKAYKAEAAKAAKE 81
   Query Match
Best Local Similarity 36.2%;
Matches 29; Conservative
   LENGTH: 434 amino acids
TYPE: amino acid
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  TOPOLOGY: circular
OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
  CITY: New York
STATE: New York
COUNTRY: USA
   New York
   US-09-864-761-36182
   ZIP: 10036
  RESULT 15
US-09-124-280A-3
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   GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
   7; Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 60
         43; Indels
   EXPRESSED IN HELA, SIGNAL = 1.3
EXPRESSED IN HEL100, SIGNAL = 0.94
EXPRESSED IN HEART, SIGNAL = 1.3
EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 36182 LENGTH: 617
         4; Mismatches
  THIRE REPERNICHION UGENE EAFRESSION ANALISIS CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT PILING DATE: 2001-05-23 PRIOR PILING DATE: 2000-06-26 PRIOR FILING DATE: 2000-06-26 PRIOR PILING DATE: 2000-06-36 PRIOR APPLICATION NUMBER: US 60/236,356 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR PILING DATE: 2000-10-04 PRIOR PILING DATE: 2000-10-04 PRIOR PILING DATE: 2000-10-04 PRIOR PILING DATE: 2001-01-30 PRIOR PILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/USO1/00665 PRIOR APPLICATION NUMBER: PCT/USO1/00665 PRIOR PILING DATE: 2001-01-30 PRIOR PILING DATE: 2000-06-30 PRIOR PILING DATE: 2000-06-31 PRIOR PILING DATE: 2000-06-31 PRIOR PILING DATE: 2000-01-30 PRIOR PILING DATE: 2001-01-30 P
  235 akpaakpvakptakpaaktaaakpaakpa 267
  61 YKAEA-----AKKAYKAEAAKAAAKEAAYEA 86
  Sequence 36182, Application US/09864761
Patent No. US20020048763A1
   PRIOR FILING DATE: 2001-01-
NUMBER OF SEQ ID NOS: 49117
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
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  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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409
   BLOSUM62
   Scoring table:
   Perfect score:
  Database :
   Sequence:
   Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | tion               | ce 64, Appl       | 64,               | 64,               | 64,              | 27,              | 10,              | 10,              | 7               | 7               | æ               | œ               | ς,              | 7                | 20                | 20                | 'n              | m               | 'n              | 40,              | 32,              | 9                | 4,              | 4               | 'n               | ı,              | 51,               | ce 51, Appl      |
|-----------|--------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|-------------------|-------------------|-----------------|-----------------|-----------------|------------------|------------------|------------------|-----------------|-----------------|------------------|-----------------|-------------------|------------------|
|           | Description        | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Seguence         | Sequence        | Sequence        | Sequence        | Sequence        | Seguence        | Seguence         | Seguence          | Seguence          | Sequence        | Seguence        | Sequence        | Seguence         | Seguence         | Sequence         | Sequence        | Sequence        | Sequence         | Seguence        | Sequence          | Sequence         |
| SUMMARIES | αI                 | US-08-460-890A-64 | US-08-167-641C-64 | US-08-460-971A-64 | US-08-462-040-64 | US-09-041-889-27 | US-08-216-894-10 | US-09-115-746-10 | US-08-216-894-2 | US-09-115-746-2 | US-08-216-894-8 | US-09-115-746-8 | US-08-346-849-2 | US-08-293-284A-2 | US-09-095-855-201 | US-09-205-426-201 | US-08-929-329-5 | US-09-041-889-3 | US-08-837-058-3 | US-09-041-889-40 | US-09-041-889-32 | US-08-993-008A-6 | US-09-041-889-4 | US-08-837-058-4 | US-08-403-379A-1 | US-08-929-414-1 | US-08-557-309B-51 | US-08-834-306-51 |
|           | Length DB          | 100 2             | 100 3             | 100 4             | 100 4            | 214 3            | 472 2            | 472 4            | 564 2           | 564 4           | 643 2           | 643 4           | 433 1           | 433 2            | 223 4             | 223 4             | 1507 3          | 222 3           | 222 3           | 158 3            | 226 3            | 56 4             | 218 3           | 218 3           | 262 1            | 262 2           | 263 2             | 263 3            |
| de        | Query<br>Match Len | 38.1              | _                 |                   |                  |                  | 33.6             |                  |                 |                 |                 |                 |                 |                  |                   |                   | -               |                 |                 |                  | 29.6             |                  | 9.              |                 | ~!               | 28.2            | .2                | 7.               |
|           | Score              | 156               | 156               | 156               | 156              | 147              | 137.5            | 137.5            | 137.5           | 137.5           | 137.5           | 137.5           | 133.5           | 133.5            | 129.5             | 129.5             | 127.5           | 127             | 127             | 121              | 121              | 119.5            | 117             | 117             | 115.5            | 115.5           | 115.5             | 115.5            |
|           | Result<br>No.      | н                 | 7                 | 3                 | 4                | S                | φ                | 7                | 80              | σ               | 10              | 11              | 12              | 13               | 14                | 15                | 16              | 17              | 18              | 19               | 50               | 21               | 22              | 23              | 24               | 25              | 56                | 27               |

| Sequence 51, Appl<br>Sequence 51, Appl<br>Sequence 62, Appl                     |                                                                               | Sequence 5, Appli<br>Sequence 54, Appli<br>Sequence 52, Appl<br>Sequence 52, Appl                 | Sequence 52, Appl<br>Sequence 2, Appli<br>Patent No. 5268270<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli |
|---------------------------------------------------------------------------------|-------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| US-08-993-674A-51<br>US-09-256-976-51<br>US-08-460-890A-62<br>US-08-167-641C-62 | US-08-460-971A-62<br>US-08-462-040-62<br>US-08-097-830E-3<br>US-08-456-112R-3 | US-08-993-008A-5<br>US-08-557-309B-54<br>US-08-834-306-52<br>US-08-993-674A-52                    | US-09-256-976-52<br>US-09-344-529-2<br>5268270-2<br>US-08-312-949-4<br>US-08-446-201-4<br>US-08-072-070-4                   |
| 4404                                                                            | 4440                                                                          | 14004                                                                                             | 449661                                                                                                                      |
| 263<br>263<br>100                                                               | 100                                                                           | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                             | 442<br>92<br>1507<br>288<br>288<br>289                                                                                      |
| 288.2<br>26.2<br>26.7                                                           | 266.7                                                                         | 255.0<br>25.0<br>25.0<br>25.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3 | 25.8<br>25.7<br>255.7<br>255.7<br>25.4<br>25.4<br>4.4                                                                       |
| 115.5                                                                           | 60000                                                                         | 106.5<br>105.5<br>105.5                                                                           | 105.5<br>105<br>104<br>104<br>104                                                                                           |
| 28<br>30<br>31                                                                  |                                                                               | 3 3 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                           | 4 4 4 4 4<br>0 1 2 6 4 8                                                                                                    |

### ALIGNMENTS

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   Sequence 64, Application US/08460971A

Sequence 64, Application US/08460971A

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
  CTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
  Length 100;
  38.1%; Score 156; DB 4; Length 100;
  38.1%; Score 156; DB 3; Length 10
55.3%; Pred. No. 3.7e-08;
tive 6; Mismatches 30; Indels
  COUNTRIT 0.5.0.

ZIP: 90071-2066

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5." Diskette, 1.44 Mb
MEDIUM TYPE: BM Compatible
CURRENT APPLICATION DATA: WISHOWS 2.0
CURRENT APPLICATION DATA: WS/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: March 20, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTONNEY, AGENT INFORMATION:
NAME: WARDLEY, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
   83
   || || || || || 62 AKAKAKAKAKAKAKA 86
  TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
TENGTH: 100 amino
   59 AKYKAEAAKKAYKAEAAKAAAKEAA
  LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
   Query Match
Best Local Similarity 55.33
Matches 47; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
  US-08-167-641C-64
   US-08-460-971A-64
   Query Match
  임
   ò
   셤
   Gaps
  1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
   Sequence 64, Application US/08167641C
| Sequence 64, Application US/08167641C
| Patent No. 6033844
| GENERAL INFORMATION:
| APPLICANT: Who, Savio L.C.
| APPLICANT: Smith, Louis C.
| APPLICANT: Smith, Louis C.
| APPLICANT: Getchalk, Stephen TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
| CORRESPONDENCES: 65
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon & Lyon STREET: 633 West Fifth Street
| STREET: 633 West Fifth Street
| STREET: Galicania COUNTY: Los Angeles
| CONTY: Los Angeles
   "Lys Ala" in positions 3 to 100 may be present or absent.
  OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
  Query Match
38.1%; Score 156; DB 2; Length 100;
Best Local Similarity 55.3%; Pred. No. 3.7e-08;
Matches 47; Conservative 6; Mismatches 30; Indels
   COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
ONDERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION ATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/UG93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburd J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
MEDISTRATION NUMBER: 32,327
  62 AKAKAKAKAKAKAKAKAKA 86
   59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
  TOPOLOGY: linear
WOLECULE TYPE: peptide
FEATURE:
  ) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-460-890A-64
   STRANDEDNESS:
  US-08-167-641C-64
  ò
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18-09-041-889-27
Sequence 27, Application US/09041889
SETILE OF INVENTION: Diagnosis, Prevention and Treatment of TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using TITLE OF INVENTION: MICROBIAL UC PANCA antigens
NUMBER OF INVENTION: MICROBIAL UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
   111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
   Query Match 35.9%; Score 147; DB 3; Length 214; Best Local Similarity 50.0%; Pred. No. 5.5e-07; Matches 47; Conservative 3; Mismatches 34; Indels 10; Gaps
  1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                               1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
  55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 535-9041
TELERHONE: (619) 535-9049
INPORMATION POR SEQ ID NO: 27:
  ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
   62 АКАКАКАКАКАКАКАКАКАКАКА 86
   US-08-216-894-10; Application US/08216894; Sequence 10, Application US/08216894; Patent No. 5879734; GENERAL INFORMATION: APPLICANT: Kirchhoff, Louis V.
  : 214 amino acids
amino acid
   SEQUENCE CHARACTERISTICS:
  , MOLECULE TYPE: peptide US-09-041-889-27
   linear
   USA
   TOPOLOGY:
  COUNTRY:
   LENGTH:
  RESULT 5
  RESULT 6
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  셤
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                             3
   7
   Gaps
                               Gaps
   1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
  ñ
   Sequence 64, Application US/08462040

Sequence 64, Application US/08462040

Patent No. 6177554

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MCLEIC ACID TRANSPORTER SYSTEMS AND
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Suite 4700

CITY: Los Angeles

COUNTRY: U.S.A.

COUNTRY: U.S.A.
   OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
   Query Match 38.1%; Score 156; DB 4; Length 100; Best Local Similarity 55.3%; Pred. No. 3.7e-08; Matches 47; Conservative 6; Mismatches 30; Indels
1 Similarity 55.3%; Pred. No. 3.7e-08; 47; Conservative 6; Mismatches 30; Indels
   COUNTITE U.S.A..

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORMED
COMPUTER: IBM COMPATIBLE
COMPATIBLE
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY,AGENT INFORMATION:
NAME: MARCH 19, 1993
ATTORNEY,AGENT INFORMATION:
NAME: MARDILES RICHARM 3.
  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 212/078
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
   59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
   100 amino acids
   TYPE: amino acid
STRANDEDNESS: single
   TOPOLOGY: linear
MOLECULE TYPE: peptide
Best Local Similarity
   US-08-462-040-64
  US-08-462-040-64
  LENGTH:
                             Matches
   ò
  8
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346 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 402
  5; Gaps
  Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAAK-AEKKEYAAAEA 59
   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPEDUBNICE ADDRESS:
ADDRESSE: Foley & Larder
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
  5
  Length 472;
  Indels
  Indels
  33.6%; Score 137.5; DB 4;
48.9%; Pred. No. 9.5e-06;
tive 11; Mismatches 29;
  SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
  33.6%; Score 137.5; DB 2;
48.9%; Pred. No. 1.1e-05;
tive 11; Mismatches 29;
  85326/102/DRLO
   .
29,768
RR: 85326/102/DRLO
   403 TKVAEAEKQKAAEATKVAEAEKQKAAEA 430
   60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 8532,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAK: (202)672-5399
   Sequence 2, Application US/08216894
Patent No. 5876734
  REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-530
TELEFAX: (202)672-539
  TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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  43, Conservative
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Best Local Similarity 48.99
Matches 43; Conservative
   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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   20007-5109
   MOLECULE TYPE:
  FILING DATE:
  TOPOLOGY:
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   US-08-216-894-2
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  Gaps
  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Polley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
ZITY: Washington, D.C.
  5;
  RESULT 7
US-09-115-746-10

Sequence 10, Application US/09115746

Sequence 10, Application US/09115746

Batent No. 6228601

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: OCESU, Kirchhoff, Louis V.

TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CONTY: Washington, D.C.
  DB 2; Length 472;
  Query Match
33.6%; Score 137.5; DB 2; Length 4
Best Local Similarity 48.9%; Pred. No. 9.5e-06;
Matches 43; Conservative 11; Mismatches 29; Indels
   SOFTWARE: PETENT RELEASING #1.25
SOFTWARE: PETENT RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMONICATION:
TELECOMONICATION: (202) 672-5399
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
  403 TKVAEAEKQKAAEATKVAEAEKQKAAEA 430
  60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
  COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acids
   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-216-894-10
  COUNTRY: USA
ZIP: 20007-5109
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  ð
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
   Query Match 33.6%; Score 137.5; DB 2; Length 643; Best Local Similarity 48.9%; Pred. No. 1.3e-05; Matches 43; Conservative 11; Mismatches 29; Indels 5
       POLYPEPTIDES FOR DIAGNOSING INFECTION WITH TRYPANOSOMA CRUZI
   POLYPEPTIDES FOR DIAGNOSING INFECTION WITH TRYPANOSOMA CRUZI
  GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPERTIDES FOR DIAGNOSING INF
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folsy & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
ALING DA
   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 85326/102/DRLO
TELEFRANCE/CONTON INFORMATION:
TELEFRANCE/CONTON INFORMATION:
TELEFRANCE/CONTON INFORMATION:
TELEFRANCE/CONTON INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNO TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: RADBRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
   519 TKVÁBÁBKOKÁABÁTKVABÁBKOKÁABÁ 546
   60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
  ZIP: 20007-5109
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
   US-09-115-746-8; Sequence 8, Application US/09115746; Patent No. 6228601
   643 amino acids
   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  TOPOLOGY: linear
MOLECULE TYPE: protein
  amino acid
   US-08-216-894-8
   LENGTH:
  RESULT 11
   g
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   ઠ
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   GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
   COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
  491 TKVAEAEKQKAAEATKVAEAEKQKAAEA 518
   491 TKVAEAEKQKAAEATKVAEAEKQKAAEA 518
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  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
  Sequence 2, Application US/09115746 Patent No. 6228601
  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 8532
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
  US-08-216-894-8

Sequence 8, Application US/08216894

Patent No. 5876734

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Otsu, Keiko
   TELERAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-09-115-746-2
   (202) 672-5300
(202) 672-5399
   RESULT 10
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5; Gaps

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61 YKAEAAKKAYKAEAAKAAAKEAAY 84
   40; Conservative
MOLECULE TYPE: protein
  TOPOLOGY: linear
MOLECULE TYPE: protein
  Best Local Similarity
Matches 40; Conserva
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  US-08-293-284A-2
      ; MOLECULE ...
US-08-346-849-2
  Query Match
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  3,
  Sequence 2, Application US/08346849
Fatent No. 5670483
GENERAL INFORMATION:
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Holmes, Todd
ITILE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
ITILE OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
   462 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 518
  Gaps
   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
  33.6%; Score 137.5; DB 4; Length 643; ilarity 48.9%; Pred. No. 1.3e-05; Conservative 11; Mismatches 29; Indels 5.
   REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
   519 TKVAEAEKOKAAEATKVAEAEKOKAAEA 546
   60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
  TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acids
TOPOLOGY: linear
 ATTORNEY/AGENT INFORMATION:
  LENGTH: 433 amino acids
TYPE: amino acid
                NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
   ; MOLECULE TYPE: protein US-09-115-746-8
   Lexington
Massachusetts
   Query Match
Best Local Similarity
   TOPOLOGY: linear
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  RESULT 12
US-08-346-849-2
   STATE:
   Matches
  셤
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Э,
  7; Gaps
  290 KEEEKKEKEKRRKWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKK-----KAK 344
  2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAEAK 60
   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAEAK 60
  GREERAL INCORNATION:

APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO Militia Drive
Query Match 32.6%; Score 133.5; DB 1; Length 433; Best Local Similarity 47.6%; Pred. No. 2e-05; Matches 40; Conservative 12; Mismatches 25; Indels 7
   Length 433;
  CITY: Leakington

STATE: Massachusetts

CONTRX: U.S.A.

ZIP: 0.2.173-4799

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: BEACHIN Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: 22-AUG-1994

FLING DATE: 22-AUG-1994

CLASSIFICATION NUMBER: US/08/293,284A

FILING DATE: 28-DEC-1992

ATORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 2.5.92

REFERENCE/DOCKET NUMBER: MIT-6008A

TELECOMMUNICATION INFORMATION:
NAME: MITCH TOWN NUMBER: MIT-6008A
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2e-05;
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  32.6%; Score 133.5;
47.6%; Pred. No. 2e-0
tive 12; Mismatches
  US-08-293-284A-2; Sequence 2, Application US/08293284A; Patent No. 5955343
   61 YKAEAAKKAYKAEAAKAAAKEAAY 84
  (617) 861-6240
   TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
   : 433 amino acids
amino acid
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Search completed: March 10, 2003, 12:30:03 Job time : 15.2405 secs
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  Sequence 201, Application US/09095855
; Patent No. 6160033
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; VOWRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA

COUNTRY: USA
   1 AKKYAKK---EKAYAKKAEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEKKEYA 55
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  Query Match 31.7%; Score 129.5; DB 4; Length 223; Best Local Similarity 54.3%; Pred. No. 2.4e-05; Matches 50; Conservative 5; Mismatches 26; Indels 11.
  ZIP: 1981.2

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: 1BM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:
  CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/97,362
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
RAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REPERRENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
  168 AAPAK-KAPAKKAATKAAPAKKAPAKKAATKA 198
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|:|||| | | ::|||| | 345 EAAKAAKKKNK-RAIRNSAKEADY 367
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SEQUEENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
  TELEFAX: 206-269-0563
   TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-095-855-201
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RESULT 15 82.09-205-426-201 ; Sequence 201, Application US/09205426 ; Patent No. 6406704

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Indels 11; Gaps
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## APPLICANT: Wateson, James D.
## APPLICANT: Wateson, James D.
## APPLICANT: Tan, Paul L. J.
## APPLICANT: Tan, Paul L. J.
## TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Ompounds of Mycobacterial Infections
## TITLE OF INVENTION: Disanceis of Mycobacterial Infections
## TITLE OF INVENTION: Disanceis of Mycobacterial Infections
## TITLE OF INVENTION: NUMBER: US/09/205,426
## CURRENT FILING DATE: 1998-12-04
## EARLIER APPLICATION NUMBER: 08/997,362
## EARLIER APPLICATION NUMBER: 08/997,362
## EARLIER PILING DATE: 1999-06-12
## EARLIER PILING DATE: 1996-08-29
## NUMBER OF SEQ ID NOS: 208
## SOFTWARE: FastSEQ for Windows Version 3.0
## SEQ ID NO 201
## INVENTION OF TANKED INCOME TANKED IN
   Query Match 31.7%; Score 129.5; DB 4; Length 223; Best Local Similarity 54.3%; Pred. No. 2.4e-05; Matches 50; Conservative 5; Mismatches 26; Indels 11.
   168 AAPAK-KAPAKKAATKAAPAKKAPAKKAATKA 198
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   ; ORGANISM: Mycobacterium vaccae US-09-205-426-201
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5.1.3
Compugen Ltd.
version = 2003 (
GenCore (c) 1993
       Copyright
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- protein search, using sw model OM protein March 10, 2003, 12:15:04 ; Search time 31.9641 Seconds
 (without alignments)
327.825 Million cell updates/sec Run on:

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Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| ٣             | 181.5 | 35.0  | 394    | N  | G85576    | membrane spanning  |
| 4             | 181   | 34.9  | 210    | N  | A25550    | histone H1 - sea u |
| S             | 179   | 34.5  | 347    | ~  | E83525    | Tola protein PA097 |
| 9             | 178   | 34.3  | 376    | N  | AG0592    | tolA protein [impo |
| 7             | 178   | 34.3  | 388    | ~  | AC0138    | colicin            |
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| 0             | 172.5 | 33.2  | 211    | ~  | A28100    |                    |
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| 11            | 170.5 | 32.9  | 248    | Н  | HSUR1P    | histone H1, gonada |
| 12            | 170.5 | 32.9  | 1701   | N  | T09127    | probable erythrocy |
| 13            | 165   | 31.8  | 220    | ~  | A28456    | histone H1.10 - ch |
| 14            | 164.5 | 31.7  | 231    | ~  | S59589    | histone H1 - Chlam |
| 15            | 164   | 31.6  | 265    | ~  | S19113    | cgcr-4 protein - C |
| 16            | 164   | 31.6  | 311    | 7  | T17698    | hypothetical prote |
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| 23            | 161   | 31.0  | 219    | N  | E60110    | repetitive protein |
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RESULT 2 F90725

| hypothetical prote | histone H1-II - Vo | polyhydroxyalkanoa | conserved hypothet | outer membrane int | histone H1.03 - ch | probable translati | histone H1 - mouse | histone H1-gamma, | histone H1 (clone | histone H1 - musco | histone H1 - mouse | histone H1.1 - Cae | histone H1 - mouse | hypothetical prote | regulatory protein |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
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| 32                 | Š                  | 683                | H7                 | ဗ                  | ä                  | E                  | Ā                  | A                 | £                 | တ                  | Ĥ                  | H                  | S                  | Ā                  | ٨                  |
| 2 82               | 2 JNO              | 2 G83              | 2 H7               | 2<br>2             | 2<br>D2            | 2<br>T             | 2 A                | 2 A2              | 2<br>T0           | 2                  | 7                  | 2                  | 2 84               | 2 AI               | 2<br>A             |
| N                  | 241 2 JNO          | ~                  | ~                  | ~                  | ~                  | ~                  | 0                  | 7                 | ~                 | 7                  | 7                  | ~                  | ~                  | 7                  | N                  |
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### ALIGNMENTS

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   A; Molecule type: DNA
A; Residues: 1-421 - LEV>
A; Residues: Gs. Rizain JM105
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: B64810
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A;Molecule type: DNA
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A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for collcins E2, E3, A, and K to reach t
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   Similarity
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A; Start codon: GTG
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Best Local Simi
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   ઠે
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  A, Experimental source: strain PAO1
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A;Molecule type: DNA
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  C; Accession: AG0592
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  155
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  ò
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  g
   ઠે
   membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain CiSpecies: Escherichia coli CiSpecies: Sistema, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G88576
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: tolA
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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
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C;Accession: A25550
R;Knowled J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an
   gend
          substrain
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membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substri
C;Species: Escherichia coli
C;Adcession: F90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yawunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90725
A;Accession: F90725
A;Accession: F90725
A;Crossion: F00725
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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   5
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   Gaps
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   56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
   AAAEAQKKAEAAAALKKKAEAAEAAAEARKKAAAEKAAADKKAAEKAAAEKAA 232
  56 AKKBAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
  11;
   11;
   35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 4.7e-05; tive 12; Mismatches 32; Indels 11
  35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 4.7e-05; tive 12; Mismatches 32; Indels 11.
  60; Conservative
  Conservative
   Best Local Similarity
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60: Conserv
  A; Gene: EC80774
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradhan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 559-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
   tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18 C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
  Fiparkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Noule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
   GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
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   6 KKAEKAYAKKAKAKAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
   58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
   краккааккраак--кааккрааккраккааккрааккаакраккааккрааккаа 208
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 «ANXO
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34.9%; Score 181; DB 2;
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Matches 58; Conservative 8; Mismatches 36;
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C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene encomal patterns of the ge
   Species: Drosophila hydei
C;Species: Drosophila hydei
C;Spacession: S51364; S34154
R;Nessen, J.; Padmanabhan, S.; Buenemann, H.
R;Nessen, J.; Padmanabhan, B.; Padmanabhan, M.
R;Nessen, J.; Padmana
  C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
   88 KLGKKKEGKSDAQKARDAAKKALAAKKKEAKEKKAARKKEKLAAKKEKTKKVK 147
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  Gaps
  sea urchin (Strongylocentrotus purpuratus)
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   Length 1390;
         Length 344;
   Length 211;
  Indels
  Indels
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A,Resean, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
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  A;Accession: S34154
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Best Local Simi
Matches 58;
  A; Gene: mst101(2)
  histone H1-beta,
   Query Match
  Best Local
  Genetics
   26
  Matches
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  C;Species: Yersinia pestis
C;C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession. AC0138
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Acons acoustic MUD:21470413; PMID:11586360
A;Status: preliminary
  4
   7;
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C;Accession: S34153
R;Nessen, J.; Heinlein, U.A.O.; Buenemann, H.
Bubmitted to the EMBL Data Library, June 1993
  54 AKAKKEAYKAEAKKYAKAAK----AEKKEYAAAEAKKAEAAK-AYKAEAAKAAAKEA 105
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  ;
10
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52.1%; Pred. No. 7.7e-05;
ive 12; Mismatches 28; Indels
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A;Status: preliminary
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  A 258
   106 A 106
  Query Match
   Local
   A;Gene: tolA
   Matches
  258
   RESULT 8
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complement. Generation of a com;
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Cipate: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
CiAccession: S5589; 862122
RiFabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone general areforement number: S59581; MUID:96120862; PMID:8590479
  A/Status: nucleic acid sequence not shown
A/Status: nucleic acid sequence not shown
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A/Molecule type: DNA
A/Residues: 1-231 <FMB>
A/Cross-references: EMBL:U16726
A/Molec: the authors did not translate the codon for residue 1
A/Molec: the authors did not translate the codon for residue 1
A/Pescription: The organization, Structure and controlling elements of Chlamydomonas histi
A/Rescription: The organization, structure and controlling elements of Chlamydomonas histi
A/Accession: S62122
A/Accession: S62
  C, Superfamily: histone H1 C; Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus F; 2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
   histone H1.10 - chicken
C;Species: Gallus gallus (chicken)
C;Daces 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 04-Mar-2000
C;Accession: A24456
R;Coles, L.S.; Robins, A.J.; Madley, L.K.; Wells, J.R.E.
J. Biol. Chem. 26., 9565-963, 1987
A;Title: Characterization of the chicken histone H1 gene complement. Generat
A;Reference number: A92655; MUID:87250632; PMID:3597432
  109 SKKPGEVKEKAPRKRTPAAKPKKPAAKKPASAAKKPKKAAAAKKSPKKAKKPAAAATKKA 168
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   64 EAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
  histone H1 - Chlamydomonas reinhardtii
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C.Species: Parechinus angulosus (angulate urchin)
C.Species: Parechinus angulosus (angulate urchin)
C.Species: Parechinus angulosus (angulate urchin)
C.Species: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 16-Feb-1997
C.Accession: A91090; A01091; A05866
R.Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang A;Contents: sequence of residues 1-84
A;Accession: A91090
A;Molecule type: protein
A;Residues: 1-248 <STR>
R;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
Eur. J. Biochem. 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang A;Accession: A91091; MUID:80156832; PMID:7363905
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R;Residues: 1-1701 KKAP>

R;Residues: 1-1701 KAP>

R;Residues: 1-1701 KA
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2
  1067 AKKLKBAAEKKQCEERAKKEKEAAEKKQCEERAKKLKEAAEKKQCEERAKKEKEBAAEKKR 1126
  120 KKAKKTSAAAKKKAKAKAAAKKAKAKAAAKRKAALAKKKAAAAKRKAAAKAKKKKK 179
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  Best Local Similarity 46.0
Matches 52; Conservative
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   Best Local
   180
  Matches
   RESULT 12
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RESULT 15
S19113
cgcr-4 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S1446
R;WakAsrchuk, ww. w., Wu., Puller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements
A;Reference number: S19113; MUD:92119224; PMID:1731966
A;Accession: S19113
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Search completed: March 10, 2003, 12:28:30 Job time : 32.9641 secs

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OM protein - protein search, using sw model

March 10, 2003, 12:15:01; Search time 24.8354 Seconds (without alignments) 182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

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Scoring table:

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112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | P19934 escherichia | P06144 lytechinus | P50600 pseudomonas | -     | -     |       | strong | -    |       | -   |          | P16401 homo sapien | Q9zhc5 mycobacteri |       | homo 88 | gallus | gallus | Q08865 volvox cart | haemop | _          | schizo | -   | -         | kleb | P09426 anas platyr | mus 1 | P10771 caenorhabdi |     | P09987 gallus gall | P50887 drosophila | 4     | 27      | P15865 rattus norv |
|-----------|----------------|--------------------|-------------------|--------------------|-------|-------|-------|--------|------|-------|-----|----------|--------------------|--------------------|-------|---------|--------|--------|--------------------|--------|------------|--------|-----|-----------|------|--------------------|-------|--------------------|-----|--------------------|-------------------|-------|---------|--------------------|
| SUMMARIES | ŒΙ             | TOLA ECOLI         | <u>r</u> rpi      |                    |       |       |       |        |      |       |     | HI ONCMY |                    | IXCSM              | CHICK | IOMAIN  | CHICK  |        |                    |        | H103_CHICK |        |     | H1G_STRPU |      |                    |       |                    |     | H1 CHICK           |                   | ELYBA | P_PSEAE | H12_RAT            |
|           | DB             | <b>.</b>           | -                 | -                  | -     | -     | -     | -      | П    | -     | н   | -        | н                  | -                  | -     | н       | _      | н      | н                  | -      | -          | ٦,     | н   | -         | H    | -                  | Ä     | -                  | -   | -                  | н                 | -     | H       | -                  |
|           | Length         | 421                | 210               | 347                | 344   | 1391  | 248   | 211    | 219  | 384   | 224 | 206      | 225                | 208                | 218   | 218     | 771    | 218    | 240                | 372    | 223        | 1403   | 211 | 217       | 139  | 217                | 218   | 207                | 220 | 217                | 299               | 232   | 352     | 218                |
| de        | Query<br>Match | 36.5               | 34.9              |                    |       | 33.0  | 32.9  | 32.7   | 31.8 | 31.5  | ä   | 。        | 30.9               | 0                  | 30.7  | 30.4    | 30.3   | 0      | 29.8               | σ      | o          | σ      | 8   | 28.9      | 28.5 | 8                  | 8     | æ                  | 8   | 28.1               | 28.1              | 27.7  | 27.7    | 27.6               |
|           | Score          | 189.5              | 181               | 179                | 175.5 | 171.5 | 170.5 | 169.5  | 165  | 163.5 | 163 | 160.5    | 160.5              | 160                | 159.5 | 158     | 157    | 156.5  | 154.5              | 153.5  | 152.5      | 151    | 150 | 150       | 148  | -                  | 147.5 | 147                | 147 | 146                | 146               | 144   | 144     | 143.5              |
|           | Result<br>No.  | п                  | 7                 | m                  | 4     | ī     | 9     | 7      | 80   | σ,    | 10  | 11       | 12                 | 13                 | 14    | 15      | 16     | 17     | 18                 | 19     | 20         | 21     | 22  | 23        | 24   | 25                 | 56    | 27                 | 28  | 29                 | 30                | 31    | 32      | 33                 |

| P95109 mycobacteri P40277 chironomus P02254 salmo trutt P40276 chironomus Q9u761 aedes aegyp P40275 chironomus P02251 oryctolagus P02251 oryctolagus P00253 homo sapien Q08864 volvox cart P12036 homo sapien P40262 chironomus P40278 chironomus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |   |
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| DBH MYCTU H1C_CHITE H1_SALTR H1B_CHITE RS6_AEDAE H1A_CHITE H1A_CHITE H1A_CHITE H1A_CHITE H1A_CHITE H1A_CHITE H1E_CHIPA H1E_CHIPA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |   |
| 2212224<br>412924<br>412924<br>412924<br>112222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>11222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1222<br>1 | • |
| 7.22.22.22.22.22.22.22.22.22.22.22.22.22                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |   |
| 142 143 1442 1442 1442 1440 1440 1440 1440 1440                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ) |
| 6 6 6 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ) |

# ALIGNMENTS

| COLI STANDARD; PRT; 421 AA.             | 1991 (Rel. 17, Creat   | -1991 (Rel. 17, Last sequence update)<br>-2001 (Rel. 40, Last annotation update) | Tola protein.<br>Tola OB CIM OB EXCC OR LKY OR R0739 | ichia coli. | la; Proteobacteria; gamma subdivision; Enterobacteriaceae; | ichia.      | axid=562;                | SEQUENCE FROM N.A. | STRAIN=JM105;<br>WRDD: 1NP-80078104. D:: MAG-2687247. | ood S.K. Webster R.E.; | and tolB    | products, components of a multistep translocation system in | Escuericnia coll.";<br>J. Bacteriol. 171:6600-6609(1989). |     | CE FROM N.A. | STRAIN=KLZ / MG1655;<br>MEDLINE=97426617: PubMed=9278503: | R., Plunkett G. III, Bloch C.A., Perna N.T., Bur | ollado-Vides J., Glasner J.D., Rode C.K., Mayhew | J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., | , Shao Y.;       | "The complete genome sequence of Escherichia coil K-12.";<br>Science 277:1453-1474(1997) | . ( | SEQUENCE FROM N.A. | =K12;       | E=97061202; PubMed=8905232; | Osnima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,<br>Themoto V. Inade T. Itch T. Valihana M. Kanai V. Kashimoto V | S. Kitagawa M. Makino K. Masuda S. Miki T. Mizobuchi K. | ., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., | G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., | ., Horiuchi T.; | "A 718-Kb DNA sequence of the Escherichia coll K-12 genome | · dam officer our in |     | · so     | E=91296736; PubMed=2068069; |             | a membrane protein involved in colicin uptake contains an | region.";   | Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991). | ון כן ן<br>מנידומית יוחדוני היסדומיר ביחדוני היסדומיר ביחדוני היסדומיר ביחדוני היסדומיר ביחדוני היסדומיר ביחדוני היסדומיר | CITCH WITH FORTUNAL CONTOCKO. | MEDLINE=9/1332/1; FUDMEQ=89/8008;<br>Deroniche P (Bavioli M Renedetti H Drilipov A Lazdungki C |
|-----------------------------------------|------------------------|----------------------------------------------------------------------------------|------------------------------------------------------|-------------|------------------------------------------------------------|-------------|--------------------------|--------------------|-------------------------------------------------------|------------------------|-------------|-------------------------------------------------------------|-----------------------------------------------------------|-----|--------------|-----------------------------------------------------------|--------------------------------------------------|--------------------------------------------------|-----------------------------------------------------------|------------------|------------------------------------------------------------------------------------------|-----|--------------------|-------------|-----------------------------|-------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------|-----------------------------------------------------------------|------------------------------------------------------------|-----------------|------------------------------------------------------------|----------------------|-----|----------|-----------------------------|-------------|-----------------------------------------------------------|-------------|---------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|
| RESULT 1<br>TOLA ECOLI<br>ID TOLA ECOLI | P19934;<br>01-FEB-1991 | 16-OCT-2001                                                                      | Tola protei                                          | Escherichia | Bacteria; P                                                | Escherichia | NCB1_Tax1D=562;<br>  [1] | SEQUENCE FR        | STRAIN=JM105;                                         | Levengood S            | "Nucleotide | their produ                                                 | J. Bacterio                                               | [2] | SEQUENCE FR  | MEDLINE=974                                               | Blattner F.                                      | Riley M., C                                      | Gregor J.,                                                | Mau B., Shao Y.; | The comple                                                                               | [3] | SEQUENCE FR        | STRAIN=K12; | MEDLINE=970                 | Oshima T.,                                                                                                                    | Kimira S.                                               | Mori H., Mo                                                     | Sampei G.,                                                 | Yano M., Ho     | "A 718-kb D                                                | DNA Reg. 3:          | [4] | DOMAINS. | MEDLINE=912                 | Levengood S | "TolA: a me                                               | extended he | Proc. Naci.                                       | [5]                                                                                                                       | WEDI TWE-071                  | MEDLINE=9/133                                                                                  |
| 5 3                                     | DAC                    | 2 52                                                                             | E 2                                                  | So          | 8                                                          | 88          | Š                        | RP                 | 2<br>2<br>3<br>4                                      | 2 2                    | RT          | RT.                                                         | R.                                                        | RN  | 젊            | 2 %                                                       | RA                                               | RA                                               | RA<br>S                                                   | A E              | X D                                                                                      | 2 2 | RP                 | RC          | X :                         | <b>8</b> 8                                                                                                                    | A A                                                     | RA                                                              | æ                                                          | KA<br>KA        | RT<br>T                                                    | RL                   | R.  | RP       | RX                          | RA          | RT                                                        | RT          | R R                                               | 2 E                                                                                                                       | 7 K                           | ¥ 6                                                                                            |

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   96 KTEAQKA-RAAAKKAKKALAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKA 154
  2 KKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAE----AKKKAKAEAKKYAKEAAKAK 57
  SMART; SM0526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
  SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE=20433737; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
   58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
  THE CONDENSATION OF
  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
  Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes of
   36; Indels
  Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                    Knowles J.A., Childs G.J.;

"Comparison of the late H1 histone genes of the sea urc
Lytechinus pictus and Strongelocentrotus purpuratus.";

Nucleic Acids Res. 14:8121-8133(1986).

-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENS

NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- SUBCELLULAR LOCATION: Nuclear.
   34.9%; Score 181; DB 1;
50.0%; Pred. No. 1.3e-05;
iive 8; Mismatches 36;
  01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
   347 AA
  HSSP, P02259, 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhTst_N.
Pfam; PP00538; linker histone; I.
Probom; PD000373; Linkerhist_N; 1.
   PRT;
   Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996).
MEDLINE=87040778; PubMed=3022245;
   MEDLINE=97113525; PubMed=8955385;
   EMBL; X04488; CAA28177.1; -.
  58; Conservative
   STANDARD;
  REVISIONS TO N-TERMINUS
  Pseudomonas aeruginosa.
  PIR; A25550; A25550.
  Local Similarity
  SEQUENCE FROM N.A.
  NCBI_TaxID=287;
   Tola protein.
TOLA OR PA0971.
  TOLA PSEAE
P50600;
   STRAIN=PAO;
   Query Match
  TOLA PSEAE
   Matches
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  ŝ
   Gaps
   Late histone H1.
Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
  1 AKKYAKKAE----KAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
  SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, PHOE
  Transport; Protein transport; Bactericcin transport; Transmembrane;
   SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
   56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
   178 AAAEAOKKAEAAAALKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKA 232
   PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
  11;
              "TolA central domain interacts with Escherichia coli poring.";
EMBO J. 15:6408-6415(1996).
  36.5%; Score 189.5; DB 1; Length 421; 53.0%; Pred. No. 6.3e-06; tive 11; Mismatches 32; Indels 11.
   Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
  A(2,4).
8B2F52B4B97C655E CRC64;
   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
  210 AA
   PRT;
  EMBL; M28232; AAA24683.1; -.
EMBL; AE000177; AAC73833.1; -.
  421 AA; 43156 MW;
  EMBL; D90713; BAA35405.1; -. PIR; JV0057; JV0057.
   BACTERIOPHAGE DNA.
   61; Conservative
  STANDARD;
  PIR; JV0057; JV0057.
PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
  34
421
310
421
278
   Local Similarity
  SEQUÊNCE FROM N.A.
  NCBI_TaxID=7653;
  TISSUE=Embryo;
Lloubes R.;
   Lytechinus.
  TRANSMEM
   SEQUENCE
   Query Match
  H1_LYTPI
  DOMAIN
  DOMAIN
  DOMAIN
  Best Loca
Matches
   RESULT 2
H. LYTPT
L. AC
AC
DT 01-0
DT 01-0
DT 15-0
DT
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Length 210;

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  4,
   Neesen J., Buenemann H., Heinlein U.A.;
"The Drosophila hydei gene Dhmstlol(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant files.";
Dev. Biol. 162:414-425(1994)
-!- FUNCTION: POSSTBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
  99 OKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158
  Gaps
   Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
  6 KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
  Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
Complete proteome.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
  -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
  -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
   SPERMATID BUNDLES.
DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
  10;
  Length 347;
   60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
   29; Indels
  38 347 PERIPLASMIC (POTENTIAL).
209 216 POLY-ALA.
347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
  POTENTIAL.
PERIPLASMIC (POTENTIAL).
POLY-ALA.
  CYTOPLASMIC (POTENTIAL)
  34.5%; Score 179; DB 1; 49.1%; Pred. No. 2.5e-05;
   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(1).
   344 AA
  17; Mismatches
   SEQUENCE FROM N.A., AND CHARACTERIZATION.
   MEDLINE=94200512; PubMed=8150205;
  EMBL; U39558; AAC44660.2; -.
   MST101(1).
Drosophila hydei (Fruit fly).
  EMBL; AE004530; AAG04360.1;
  Conservative
   STANDARD;
  opportunistic pathogen."
Nature 406:959-964(2000)
  16
37
347
216
  Similarity
  (BY SIMILARITY)
  (Potential).
   Muscomorpha; Eph
NCBI_TaxID=7224;
  54;
   MST1 DROHY Q08695;
  TRANSMEM
  SEQUENCE
   MST101(1)
  Query Match
Best Local (
  DOMAIN
  DOMAIN
   DROHY
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   ر
د.
   SPENNALLY.
-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
   58 337 19 X 16 AA APPROXIMATE TANDEM REPEATS OF K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X. 344 AA; 37793 MW; 24C65D2510387E2A CRC64;
   Indels 17; Gaps
   65 akkekeaaekkkcaeaakkekeaaekkkcaeaakkekeaaekkkcaeaakkekekaaekkk 124
  Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoplera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  1 AKKYAKKAEK----AYAKKAKAKAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
  50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
  "Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended abha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.";

Eur. J. Blochem. 225:1089-1095(1994).

-I- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.

-I- SUBCELLULAR LOCATION: Cytoplasmic.

-I SIBCELLULAR LOCATION: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
  Length 344;
  DB 1;
   Pred. No. 4.2e-05;
8; Mismatches 35;
  01-FEB-1995 (Rel. 31, Created)
10-FRB-1995 (Rel. 31, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
   Ä
  33.8%; Score 175.5; 49.2%; Pred. No. 4.2
   PRT; 1391
  or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A., AND CHARACTERIZATION
   PIR; S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
Sperm, Repeat; Multigene family.
   MEDLINE=95045538; PubMed=7957199;
  EMBL; X73481; CAA51876.1; -.
   EMBL; X73480; CAA51875.1; -.
   Ouery Match
Best Local Similarity 49.2
Matches 58, Conservative
   STANDARD;
  PIR; S34154; S34154.
  NCBI_TaxID=7224;
  SPERMATIDS
   REPEATS
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   MST101(2)
   SEQUENCE
  Sperm; DOMAIN
  RESULT 5
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120 KKAKKTSAAAKAKKAKAAAAKKARKAKAAAKRKAALAKKKAAAAKRKAAAKAKKKKKK 179
   KA--EAKKYAK------AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
  01-APR-1990 (Rel. 14, Created)
EMBL; M20314; AAA30052.1; -.
  55; Conservative
  STANDARD;
  STANDARD;
   , A28100; A28100.
  Query Match
Best Local Similarity
  Strongylocentrotus.
   SEQUENCE FROM N.A.
   NCBI_TaxID=7668;
  CHICK
  STRPU
  RESULT 8
H110_CHICK
ID H110 C
   62
  Matches
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  1068 AKKLKEAAEKKOCEERAKKEKEAAEKKOCEERAKKLKEAAEKKOCEERAKKEKEAAEKKR 1127
                   MEDLINE-80156832; PubMed-7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
  Gaps
  "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and the entire primary structure.";

Eur. J. Biochem. 104:567-578(1980).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
  1 AKKYAKKAEKAY----AKKAKAKAKAKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
   "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
   SMART; SM06526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
  50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
  15;
  41; Indels 11;
  DB 1; Length 1391;
  32.9%; Score 170.5; DB 1; Length 248; 46.0%; Pred. No. 6.7e-05; Live 9; Mismatches 41; Indels 11.
   Histone H1, gonadal.
Parechinus angulosus (Angulate sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
  Query Match 33.0%; Score 171.5; DB 1; Length 1: Best Local Similarity 46.2%; Pred. No. 0.00022; Matches 54; Conservative 11; Mismatches 37; Indels
  MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt
Wittmann-Liebold B.;
  26387 MW; 1B25B3F136541947 CRC64;
   -i- TISSUE SPECIFICITY: SPERM.
-i- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; A02586; HSURIP.
  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
  248 AA
FlyBase; FBgn0020733; Dhyd\mst101(2)
   K -> R.
  cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
  InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
  PRT;
   Best Local Similarity 46.0
Matches, 52; Conservative
  STANDARD;
  248 AA;
   SEQUENCE OF 80-248.
  HSSP; P02259; 1HST
   SEQUENCE OF 1-84.
  NCBI_TaxID=7658;
  21-JUL-1986
21-JUL-1986
   Parechinus
  H1 PARAN
  SEQUENCE
  Query Match
   VARIANT
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2 KKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAY 61

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   4.
   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
  MEDLINE-88246461; PubMed-2837660;
Lai Z.-C., Ghilds G.;
"Characterization of the structure and transcriptional patterns of
the gene encoding the late histone subtype HI-beta of the sea urchin
  Gaps
   88 KLGKKKEGKSDAQKAPDAAKKAKLAAKKKEAKEKKAARSKAKKEKLAAKKASKKTTKKVK 147
  3 KYAKKAE-KAYAKKA--KAAKEKKAYAKKEAKAYKAAEAK-KKAKAEAKKYAKEAAK--- 55
   HSSP, P02259; IHST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR001316; Linkerhist_N.
InterPro; IPR00318; Linkerhist_N.
Pr0Dom; PD000373; Linkerhist_N; 1.
SMART, SMOS26; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
  Q.
  6
180 KAAKKAKKPAKKSPKKAKKPAKKSPKKKAKRSPKKAKKAAGKRKPAAKKARR 232
   --AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
  Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844 (1988)
-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
  DB 1; Length 211;
  41; Indels
  SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
  32.7%; Score 169.5; DB 1
48.7%; Pred. No. 6.9e-05;
iive 8; Mismatches 41
  01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-beta, late embryonic.
   P08286;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
   211 AA
   219 AA
   44444
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Query Match
   CHAIN
  SIGNAL
  REPEAT
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   3,
                    Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
   8; Gaps
  1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEA----KAYKAAEAK---KKAKAEAKKYAKEA 53
   Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
   MEDLINE-87250632; PubMed-3597432;

MEDLINE-87250632; PubMed-3597432;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

"Characterization of the chicken histone H1 gene complement.

Generation of a complete set of vertebrate H1 protein sequences.";

J. Biol. Chem. 262:9656-9663(1987).
   MEDLINE=98060905; PubMed=9396815;
MEDLINE=98060905; PubMed=9396815;
Schwarz S., Hess D., Jost J.P.;
"The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists of histone H1 subtypes which are truncated at the C-terminus.";
Nucleic Acids Res. 25:5052-5056(1997).
-! FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-! SUBCELLULAR LOCATION: Nuclear.
-! SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
Histone H1.10 (Mcthylated DNA binding protein-2-H1) (MDBP-2-H1). Gallus gallus (Chicken).
  54 AKAKKEAYKAEAKKYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
   Length 219;
   Query Match 31.8%; Score 165; DB 1; Length 21 Best Local Similarity 46.4%; Pred. No. 0.00014; Matches 52; Conservative 11; Mismatches 41; Indels
   ACETYLATION (BY SIMILARITY).
  Treponemal membrane protein B precursor (Antigen tmpB).
   109 GLOBULAR.
21872 MW; A944DF6C0D3048AE CRC64;
   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=162;
   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
   384 AA
   EMBL; M17018; AAA48788.1; -.
PIR; A28456, A28456.
HSSP; P08287; LGHC.
InterPro; IPR001386; Histone_H1/H5.
   Pfam; PF00538; linker histone; 1.
ProDom; PD000373; Linkerhist N; 1.
  STANDARD;
   SMART; SM00526; H15; 1.
   Treponema phagedenis.
  219 AA;
  NCBI_TaxID=9031;
  Acetylation.
  TMPB TREPH P29720;
  INIT MET
MOD RES
DOMAIN
SEQUENCE
  TMPB_TREPH
   RESULT
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   3
                              Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991).

-i- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
   POTENTÏAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
   1-16.
1-17.
6 x 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
A-A-E.
  Gaps
   KKYAK-KAEKAYAKKAKAKEK----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKE--AA 54
   7;
  240 KAAEEAAARKAABEBAARKAAEBEBAARIAABEBBAARKAAEBBAARKAABBALY 292
   KAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAY 107
   Length 384;
   Indels
  6E94CBC74294DE8C CRC64;
  LARGE MOLECULES.
--- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
--- SIMILARITY: TO TMPB OF T. PALLIDUM.
  DB 1;
   42;
   ; Score 163.5; DB 1
; Pred. No. 0.00026;
12; Mismatches 42
   Ā
   224
  Antigen; Outer membrane; Repeat; Signal.
   PRT;
   13.
STRAIN=Kazan 5;
MEDLINE=91372983; PubMed=1894368;
  4.7.6.
   ED]
  01-AUG-1988 (Rel. 08, Created)
  42677 MW;
   EMBL; M58563; AAA27480.1; -.
  31.5%;
  46.08;
   Conservative
   STANDARD;
   PIR; B43592; B43592
  Local Similarity
tes 52; Conserv
  384 AA;
  166
171
176
181
181
191
191
196
206
206
211
211
  HIL CHICK
ID HILL CHICK
AC P08287;
DT 01-AUG-1988
   REPEAT
REPEAT
SEQUENCE
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   TISSUE=Spleen;
MEDLINE=90130391; PubMed=2613692;
Ohe Y., Hayashi H., Iwai K.;
"Human spleen histone Hl. Isolation and amino acid sequences of three minor variants, Hla, Hlc, and Hld.";
  105 AKKPAKKAAAPKAKKVAAKKPAAAKKPKKVAAKKAVAAKKSPKKAKKPATPKKAAKSPKK 164
  Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
  1 AKKYAK-----KAEKAYAKKAKAAKEKKAYAKKEAKAYKAAAEAKKKAKAEAKKYAKEAAK 55
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  SEQUENCE FROM N.A.

MEDLINE=85264847; PubMed=6443128;

Mezquita J., Connor W., Winkfein R.J., Dixon G.H.;

Man Hi histone gairdnerii).";

J. Mol. Bvol. 21:209-219(1988).

-I- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- SUBCELLULAR LOCATION: Nuclear.
  30.9%; Score 160.5; DB 1; Length 206; 47.7%; Pred. No. 0.00025; tive 9; Mismatches 35; Indels 13.
                            Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
  165 VKKPA--AAAK.---KAAKSPKK.---ATKAAKPKAAKPKAAKAAPKK 205
  56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
  1 ACETYLATION (BY SIMILARITY)
100 GLOBULAR.
20672 MW; 72C440798066716C CRC64;
   Last sequence update)
Last annotation update)
  Ą
   225
  InterPro; IPR001386; Histone H1/H5.
  Pfam; PF00538; linker histone; 1.
ProDom; PD000373; Linkerhist N; 1.
SMART; SM00526; H15; 1.
   H15_HUMAN STANDARD; 1
P16401; 014529; 01-AUG-1990 (Rel. 15, Created)
16-OCT-2001 (Rel. 40, Last sequine-OCT-2001 (Rel. 40, Last ann
   EMBL; X02624; CAB37646.1; -.
  Histone H1.5 (Histone H1a)
  Conservative
  PIR; A02584; HSTR1R.
HSSP; P08287; 1GHC.
   27 1
206 AA;
   Homo sapiens (Human)
  Local Similarity
  SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
  NCBI_TaxID=8022;
  Acetylation.
   52;
  INIT MET
  SEQUENCE
   Query Match
  SEOUENCE
   Matches
  RESULT 12
H15_HUMAN
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  PACCOCO O DATA TO DATA
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  5
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
  112 SKKPGEVKEKAPKKKASAAKPKKPAAKKPAAAKKPKAVAVKKSPKKAKRPAASATKKS 171
  Wodak S.J., Hallenga K., Wyns L.;
"Homo- and heteronuclear two-dimensional NMR studies of the globular
domain of histone H1: sequential assignment and secondary
   Gaps
   1 AKKYAKKAEKAYAKKAKAKAKEKK-----AYAKKEAKAYKAAEAKKKAKAEAKKYAKEA 53
  Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
   Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Characterization of the chicken histone Hi gene complement.
Generation of a complete set of vertebrate Hi protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
   STRUCTURE BY NMR OF 40-113.
MEDLINE-94032251; Pubmed-8218199;
Cerf C., Lippens G., Muyldermans S., Segers A., Ramakrishnan V.,
   Biochemistry 32:11345-11351(1993).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
  8
   AKAKKEAYKAEAKKYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
   31.4%; Score 163; DB 1; Length 224;
larity 43.8%; Pred. No. 0.00019;
Conservative 13; Mismatches 42; Indels
   ACETYLATION (BY SIMILARITY)
  D3D057CB97865CAF CRC64;
   Oncorhynçhus mykiss (Rainbow trout) (Salmo gairdneri).
  -i- SUBCELLULAR LOCATION: Nuclear.
     (Rel. 08, Last sequence update) (Rel. 38, Last annotation update)
   (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
   206 AA
   GLOBULAR
  InterPro; IPR001386; Histone H1/H5. Pfam; PF00538; linker histone; 1. ProDom; PD000373; Linkerhist_N; 1.
  SEQUENCE FROM N.A.
MEDLINE=87250632; PubMed=3597432;
  22397 MW;
  EMBL; M17019; AAA48789.1; -. PIR; B28456; B28456.
   Acetylation; 3D-structure.
                              15-JUL-1999 (Rel. 38, Lat
Histone Hl.11L.
Gallus gallus (Chicken).
   STANDARD;
  SMART; SM00526; H15; 1
  224 AA;
   Similarity
01-AUG-1988 (Rel.
   NCBI_TaxID=9031;
   P06350;
01-JAN-1988
  01 - JAN-1988
15-JUL-1999
Histone H1.
  structure.";
  49;
  SEQUENCE
   Query Match
  ONCMY
  INIT MET
  Local
  Gallus
   DOMAIN
   RESULT 11
H1_ONCMY
ID__H1_ON
AC PO635
DT 01-JA,
DT 15-JU
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  Matches
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Gaps

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01-AUG-1988
01-AUG-1988
  HIIR CHICK
P08288;
   15-JUL-1999
  SEQUENCE
   Query Match
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  ŝ
   118 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 175
  7; Gaps
  ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
  1 AKKYAKKAEKAYAKKAKAKAKAYAKKEAKAYKAA-----EAKKKAKAEAKKYAKEAAK 55
   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
  STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
MEDLINE=99110209; PubMed=9894918;
"Lee B.H., Mirugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium smegmaris.";
                    Albig W., Meergans T., Doenecke D.; "Characterization of the {\rm Hl.5~gene~completes} the set of human {\rm Hl.5}
   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
   DB 1; Length 225;
  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
. (Rel. - un homolog (Histone-like protein) (Hlp)
  56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
   44; Indels
   0 0 ACETYLATION.
1 1 ACETYLATION.
215 217 MISSING (IN REF. 1).
225 Aa; 22449 MW; 26CD4ALE5D463CDA CRC64;
   Score 160.5; DB 1
Pred. No. 0.00027;
7; Mismatches 44
   Ą
   InterPro; IPR001386; Histone H1/H5. Pfam; PP00538; linker histone; 1. PRINTS; PR00624; HISTONEHS.
  MEDLINE=97183654; PubMed=9031620;
   16-OCT-2001 (Rel. 40, Last anno
DNA-binding protein HU homolog
   30.9%;
   EMBL; X83509; CAA58498.1; -. EMBL; Z98744; CAB11421.1; -.
  Matches 51; Conservative
  STANDARD;
   Mycobacterium smegmatis.
   Gene 184:141-148(1997).
  HSSP; PO8287; 1GHC.
Genew; HGNC:4719; H1F5.
MIM; 142711;
   JX0087; JX0087.
   Similarity
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=1772;
  Q9ZHC5;
16-OCT-2001
   Acetylation.
   HUP OR HLP
  DBH MYCSM
  CONFLICT
   Query Match
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   'n.
Gen. Genet. 260:475-479(1998).
FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
   Histone Hi.11R.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
   111 AKKAAKKAP---AKKAAAKKTATKAAAKKAPAKKAA-----TKAPAKKAATK-APAKKAA 161
   14; Gaps
   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAAKKKEA 60
  Generation of a complete set of vertebzate H1 protein sequences.";
J. Biol. Chem. 262.9656-963(1987).
-!- FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF WOLLECSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
  Pred. No. 0.00027;
3; Mismatches 31: 7-7
   SEQUENCE FROM N.A.
MEDLINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
"Characterization of the chicken histone H1 gene complement.
   InterPro; IPR000119; Bac_DNAbind.
Propon; PD00216; Bac_DNA binding; 1.
Probom; PD000045; Bac_DNAbind; 1.
SMART; SM00411; BHL; I.
PROSTIE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
DNA-binding; DNA condensation; Repeat.
  DEGENERATE REPEATS REGION.
   61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEA 105
  162 ТКАРАККААТКАРА-ККАААКАРАККА----АТКАРАККАААККА 201
  (Rel. 08, Created)
(Rel. 08, Last sequence update)
(Rel. 38, Last annotation update)
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  208 AA; 21230 MW;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  'n
  Ohe Y., Hayashi H., Iwai K.; "Human spleen histone H1. Isolation and amino acid sequence of a main
   109 SKKPGEGLEKAPKKKASAAKPKKAAAKKPAAAAKKPKKAVAVKKSPKKAKPAASATKKS 168
                  PIR; C28456; C28456.
HSSP; P08387; 1GHC.
InterPro; IPR001386; Histone H1/H5.
Probom; PD00637; Linker histone; 1.
Probom; PD00037; Linkerhist N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
  Gaps
  SEQUENCE FROM N.A. Medel916825; MEDLINE-92009931; PubMed=1916825; Ablud W. Kardalinou E., Drabent B., Zimmer A., Doenecke D.; "Isolation and characterization of two human H1 histone genes within
  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKK---EAKAYKAAEAKKKAKAEAKKYAKEAAKAK 57
  Eukaryota, Metazoa;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
NCBI_TaxID=9606;
   clusters of core histone genes.";
Genomics 10:940-948(1991).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: THIS VARIANT ACCOUNTS FOR 60% OF HISTONE H1.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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  58 KEAYKAEAK-KYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
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16-CCT-2001 (Rel. 40, Last annotation update)
Histone H1.4 (Histone H1b).
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MEDLINE=87057092; Pubmed=3782055;
   218 AA; 21672 MW;
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J. Biochem. 100:359-368(1986).
  EMBL; M60748; AAA63187.1; -.
EMBL; M17020; AAA48790.1;
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PIR; C40335; C40335.
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Genew, HGNC: 4718; HIF4.
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   H14 HUANN
H14 HUANN
H17 HUANN
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108 KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA--G 165
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Probom; PD000373; Linkerhist_N; 1.
SNART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family; Acceylation; Methylation.
INIT_MET 0 0 0 ACCEYLATION.
MOD_RES 1 1 ACCETYLATION.
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  166 AKKAKSPKKAKARAKPKKAPKSPAKAKVKPKAAKPKTAKPKAAKPKKAA 214
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25 25 METHYLATION (PARTIAL).
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InterPro; IPR001386; Histone_H1/H5
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Search completed: March 10, 2003, 12:17:11 Job time : 25.8354 secs

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  Q937K4
Q937K4;
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   March 10, 2003, 12:15:01 ; Search time 57.7194 Seconds
  (without alignments)
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   1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109
  671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
  671580 seqs, 206047115 residues
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   protein search, using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_bacteria:*
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  sp_mammal:*
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   Scoring table:
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Maximum DB 8
   OM protein
  Sequence:
   Searched:
   Database
   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Q937k4 erwinia chr<br>Q94wx1 pseudomonas<br>Q8t568 plasmodium<br>Q8x46 salmonella<br>Q8x861 salmonella<br>Q8x801 salmonella<br>Q8x801 salmonella<br>Q8x707 ralstonia s<br>Q9m70 pasteurella<br>G1164 plasmodium<br>Q13976 chlamydomon<br>Q1195 drosophila<br>Q95818 drosophila<br>Q95818 drosophila<br>Q95818 drosophila<br>Q95818 drosophila<br>Q45370 bordetella |
|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES                     | 0937K4<br>099WX1<br>08T5C8<br>08T5C8<br>08X2GT6<br>08X8GT6<br>08X8GT2<br>08X8GT2<br>08XW7<br>09164<br>001164<br>001164<br>001164<br>001195<br>001395<br>095518<br>095518                                                                                                                                                                                           |
| *<br>Query<br>Match Length DB | 395 2 375 2 375 2 375 2 376 16 376 2 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                           |
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| Score                         | 190.52<br>190.53<br>190.53<br>184.55<br>178<br>178.51<br>170.53<br>166.53<br>166.53<br>166.53                                                                                                                                                                                                                                                                      |
| Result<br>No.                 | 1 1 2 2 4 8 8 7 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                            |

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| Q26947 trypanosoma | Q9kr10 vibrio chol | Q9at18 lens culina | Q9zr20 pisum sativ | Q9at22 lathyrus sa | Q9sxq8 pisum sativ |           |      | Q9at23 pisum sativ |      | Q9at24 pisum sativ |      |           |           |           | Q9at19 lens culina | O83483 treponema p | Q9v6s7 drosophila | Q23784 chironomus | O65795 triticum ae | Q9xhl9 triticum ae | Q52088 pseudomonas | Q8t5c9 plasmodium | Q93901 caenorhabdi | Q92a67 listeria in | Q9y1p8 plasmodium | O18319 chironomus | . Q9uanl drosophila | Q26938 trypanosoma |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|------|--------------------|------|--------------------|------|-----------|-----------|-----------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|---------------------|--------------------|
| 5 026947           | 16 Q9KR10          | 10 Q9AT18          | 10 Q9ZR20          | 10 Q9AT22          | 10 Q9SXQ8          | 10 Q9AT21 |      | 10 Q9AT23          |      |                    |      | 13 Q90ZD7 | 16 Q9HUC3 | 10 Q9FP71 | 10 Q9AT19          | 16 083483          | 5 Q9V6S7          | 5 Q23784          |                    | 10 Q9XHL9          | 2 Q52088           | 5 Q8T5C9          | 5 Q93901           | 16 Q92A67          | 5 Q9Y1P8          | 5 018319          | 5 Q9UAN1            | 5 Q26938           |
| 1128               | 356                | 293                | 295                | 295                | 297                | 306       |      |                    |      |                    |      |           |           | 755       | 293                | 369                | 607               | 243               | 288                |                    | 298                | 1671              | 208                | 243                | 845               | 233               | 312                 | 1052               |
| 31.3               | 31.2               | 31.1               | 31.1               | 31.1               | 31.1               | 31.1      | 31.0 | 30.9               | 30.4 | 30.4               | 30.4 | 30.1      | 29.8      | 29.8      | 29.7               | 29.6               | 29.1              | 28.9              | 28.9               | 28.6               | 28.5               | 28.5              | 28.3               |                    |                   |                   |                     |                    |
| 162.5              | 162                | 161.5              | 161.5              | 161.5              | 161.5              | 161.5     | 161  | 160.5              | 158  | 158                | 158  | 156       | 154.5     | 154.5     | 154                | 153.5              | 151               | 150               | 150                | 148.5              | 148                | 148               | 147                | 147                | 146.5             | 146               | 146                 | 146                |
| 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23        | 24   | 25                 | 56   | 27                 | 28   | 29        | 30        | 31        | 32                 | 33                 | 34                | 35                | 36                 | 37                 | 38                 | 39                | 40                 | 41                 | 42                | 43                | 44                  | 45                 |

## ALIGNMENTS

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Gaps
  1 AKKYAKKAEKAYAK-----KAKAAKEKKAYAKKEAKAYKAAEAKKKAK-------43
   44 AEAKKYAKEAAKAKKEA---YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYK--AEAA 98
   Erwinia chrysanthemi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
  22;
   Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "characterization of the Erwinia chrysanthemi tol-pal genes."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ297885; CAC82708.1; - SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
395 AA
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Matches 62; Conservative
PRELIMINARY;
  KAAAKEAAYEA 109
   [1]
SEQUENCE FROM N.A.
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   Query Match
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"Evolutionary relationships of conserved cysteine-rich motifs in
  (TrEMBLrel. 20, (TrEMBLrel. 20,
   PRELIMINARY;
  PRELIMINARY;
   Nature 413:852-856(2001)
   Local Similarity
   Complete proteome. SEQUENCE 407 AA;
  NCBI_TaxID=602;
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  1377 RKA 1379
  Q8X965
Q8X965;
01-MAR-2002 (
01-MAR-2002 (
  107 YEA 109
  01-JUN-2002
   01-MAR-2002
  01-MAR-2002
   Salmonella.
  Query Match
   Q8ZQT6
   Best Loca
Matches
   196
   RESULT 4
Q8ZQT6
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Q8X965
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   Gaps
  Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
  5 AKKAEKAYAKKAKAAK----EKKAYAKKEAKAYKAAE-----AKKKAKAEAKKYAKEAA 54
   55 K--AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
   Rodriguez-Herva J.J., Ramos J.;
Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
"Dacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB550780.1; --
InterPro; IPR001386; Histone HI/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 372 AA; 40133 MW; 87F49785ECC3COBC CRC64;
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Pseudomonas.
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  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
   Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
   Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Last annotation update)
  STRAÎN=SALVADOR;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
   372 AA.
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   Created)
  Created)
   PRT;
  11 envelope.";
Bacteriol. 178:1699-1706(1996)
   STRAIN=MT-2;
MEDLINE=96422022; PubMed=8824639;
   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
  01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
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nes 59; Conserv
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  SEQUENCE FROM N.A
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   STRAIN=MT-2;
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  09WWX1;
                                       Q9WWX1
  Q8T5C8
  MAEBL.
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1262 АККАЕЕ--АRКАЕБАККАЕБАRКАБАAККABAARKABAAKKABARKAEBARKAEBARKABARKA 1319
   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Bun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
   51 KEAAKAKKEAYKAEAKKYAKAKAKEYKEYAAAEAKKAEAAK----AYKAEAAKAAAKEAA 106
  23; Gaps
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  59 EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA 109
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
   DB 16; Length 407;
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  Indels
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  2534352116602D75 CRC64;
  Last sequence update)
Last annotation update)
adhesive molecules of malaria parasites.";

Mol. Biol. Evol. 0:0-0(2002).

EMBL, 8x042083; AAL10508.1;

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   5 AKKAEKAYAKKAKAAKE----KKAYAKKEAKAYKAAEAKKKA
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InterPro; IPR000104; Antifreeze_1.
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Matches 63;
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SEQUENCE TISE231; PubMed=11258796;

MEDINRE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Tobe T.,

Ida T., Takami H., Honda T., Sanagawa H.;

Namara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

In Namara S., Ag55075.1; -.

RMBL; AP0005523; BAB34197.1; -.

REMBL; AP0005531; BAB34197.1; -.

RINTE; PRO3081, ANTIFREEZEI.
   5
  Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.W., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
  32; Indels 11; Gaps
   1 AKKYAKKAE----KAYAKKAKAAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
   "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
  STRAIN=0157:H7 / EDL933 / ATCC 700927;

BEDLINE=21074935; PubMed=11206551;
Perna NT., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TOLA OR Z0907 OR ECS0774.
  56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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STY0793.
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  RESULT 6
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MEDINE-21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.E.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Mature 413:251-527(2001).
BMBL, AJ414146; CRG89566.1; -
InterPro; IPR000104; Antifreeze 1.
  54 AKAKKEAYKAEAKKYAKAAK-----AEKKEYAAAEAKKAEAAK--AYKAEAAKAAKEA 105
  1 AKKYAKKAEKAYAKKAKAAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60
  Gaps
  KKYAKKAEKAYAKKAKAAKEKK-----AYAKKEA-KAYKA-AEAKKKAKAEAKKYAKEA 53
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
  "Complete genome sequence of a multiple drug resistant Salmonella
   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  10;
  18;
  34.3%; Score 178; DB 16; Length 388; 52.1%; Pred. No. 7.6e-05; tive 12; Mismatches 28; Indels 18
  34.3%; Score 178; DB 16; Length 376; 52.3%; Pred. No. 7.4e-05;
   61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAA---KEAAYE 108
  376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
  388 AA; 40424 MW; 81447B04B30A7E7C CRC64;
  Pred. No. 7.4e-
10; Mismatches
   388 AA
  Tola colicin import membrane protein TOLA OR YPO1123.
   PRT;
   enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL, AL667268; CAD05209.1; -.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
   STRAIN=CO-92 / BIOVAR ORIENTALIS;
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Les 58, Conservative
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   Complete proteome. SEQUENCE 376 AA;
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  Similarity
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  Yersinia pestis
  NCBI_TaxID=632;
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7;

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InterPro; IPR000533; Tropomyosin.
PRINTS, PR00194; TROPOMYOSIN.
Complete preteome.
SEQUENCE 389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
  CH1. Chlamydomonas reinhardtii.
  (TrEMBLrel. 0 (TrEMBLrel. 0 (TrEMBLrel. 2
  PRELIMINARY;
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HSSP; P19934; 1TOL
  SEQUENCE FROM N.A.
  NCBI_TaxID=73239;
   NCBI_TaxID=3055;
  01-NOV-1996 (
01-NOV-1996 (
01-MAR-2002 (
Histone H1.
   01-AUG-1998
01-OCT-2000
  Eukaryota;
   061164;
   061164
   939576
   RESULT 10
   RESULT 11
  039576
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   8;
   50 AKEAAKAKKEAYKAEAKKYAKAAK--AEKKEYAAAEAKKAEAAKAYKAE-AAKAAAKEAA 106
   Gaps
   1 AKKYAKKAEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAK---KKA----KAEAKKY- 49
  MEDLINE=21145866; PubMed=11248100;
Max B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
Cómplete genomic sequence of Pasteuralla multocida Pm70.";
Proc. Natl. Acod Sci. D8:3460-3465(2001).
EMBL: Amo6136; AAK03052.1; -
  Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
   19;
   Score 176.5; DB 16; Length 200;
Pred. No. 5.2e-05;
5; Mismatches 32; Indels 19;
   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
  200 AA; 19279 MW; D3831B590510272D CRC64;
  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Probable histone H1 protein.
RSC2793 OR RS00453.
  Created)
Last sequence update)
Last annotation update)
  200 AA
  389 AA
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  PRT;
   STRAIN=GM11000;
MEDLINE=21681879; Pubmed=11823852;
   EMBL; AL646071; CAD16500.1; -.
InterPro; IPR00104; Antifreeze_1.
InterPro; IPR003993; treacle.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01503; TREACLE.
   Query Match
Best Local Similarity 54.5%;
Matches ' 67; Conservative
   01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
  PRELIMINARY;
   PRELIMINARY;
  Pasteurella multocida
  Complete proteome.
SEQUENCE 200 AA;
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   SEQUENCE FROM N.A.
   Ralstonia.
NCBI_TaxID=305;
  NCBI_TaxID=747;
   TOLA OR PM0968
  107 YEA 109
   157 KKA 159
  STRAIN=PM70;
  08XVN7
   09CM70
                       RESULT 8
Q8XVN7
ID Q8XV
  RESULT 9
Q9CM70
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  SEQUENCE FROM N.A. MEDLINES 9623, Park P.B., Cornelius T., Schmitt R., Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R., "The organization structure and regulatory elements of Chlamydomonas
   1205 AKKAEEE-RKKAEAVK-KAEEAKKKAEAKKAEERKK-KAEAAKKALERKKKSEAAKKAL 1261
   145 KOAEEAKAKOLAEAAKLKAEAEAKRLAALAKOAEEEAKAKAAEEAKRKAEKAKAEAEAKA 204
   9; Gaps
  5; Gaps
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Chlamydomonadaceae, Chlamydomonas.
  57 KKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
  205 KVEKAKAERAEAKVKAEKAKAERAKAKAEKAKAERAKAEKAKAEAKAKAEAKAKADEAAQRKA 257
  Length 1701;
  DB 16; Length 389;
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MEDLINE=88115903; PubMed=9448314;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
"A family of chimeric erythrocyte binding proteins of malaria
parasites.";
  Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
   6 KKAEKAYAKK-AKAAKEK-KAYAKKEAKAYKAAEAKKKAKA--EAKKYAKEA
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Matches 55; Conservative 18; Mismatches 31; Indels
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32.9%; Score 170.5; DB 5; Length
Best Local Similarity 53.5%; Pred. No. 0.00091;
Matches 54; Conservative 11; Mismatches 31; Indels
   Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
EMBL; AF031886; AAC05366.1; -.
SEQUENCE 1701 AA; 199268 MW; EDA8E2DEFD87CE8A CRC64;
   Last sequence update)
Last annotation update)
  Last sequence update)
Last annotation update)
   64 EAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
   PRT; 1701
   Created)
   Created)
  PRT;
   Erythrocyte binding protein. MAEBL.
   01,
20,
   (TrEMBLrel. 07, (TrEMBLrel. 15,
   01-AUG-1998 (TrEMBLrel. 07,
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619 AA

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PAU OR CG6544.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
  391 OKAAEEAKALKAAEDAAOKAAEEARLABEAAAOKVABEAAQKAAEEARLAEEAAAOKAAE 450
  ------ EKKEYAAAEAKKAEAAKAYKA-- 95
  9 EKAYAKKAKARAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK-AKKEAYKAE--A 65
   SEQUENCE FROM N.A.
MEDLINE=92119224; PubMed=1731966;
Wakarchuk W.W., Muller F.W., Beck C.F.;
"Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements of directly repeated sequence motifs.";
Plant Mol. Biol. 18:143-146(1992).
EMBL, X17208; CAA35080.1; -.
  Ctapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AVGO997; AAL28545.1; -. Flybase; FBGN0020439; EMBL/GenBank/DDBJ GAGABASCE CRC64;
   Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
  32.1%; Score 166.5; DB 5; Length 619; 41.0%; Pred. No. 0.00067; ive 16; Mismatches 30; Indels 33;
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(TremBlrel. 19, Last sequence update)
(TremBlrel. 20, Last annotation update)
  Last sequence update)
Last annotation update)
  Created)
   PRT;
   01-NOV-1996 (TrEMBLrel. 01, Ci
01-NOV-1996 (TrEMBLrel. 01, La
01-DEC-2001 (TrEMBLrel. 19, La
CGCr-4 product (Fragment).
  Chlamydomonas reinhardtii.
   Local Similarity 41.0%
tes 55; Conservative
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  1 AKKYAKKAEKA---
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   01-DEC-2001 (
01-DEC-2001 (
01-MAR-2002 (
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                    Q95S18
Q95S18;
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   039598
   Matches
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  RESULT 14
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   54 ----AKAKKEAYKAEAKKYAKAAKAEKKEYAAAE---AKKAEAAK---AYKAEAAKAAAK 103
   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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  18;
histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
   13;
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  58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAAYE 108
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Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
   29; Indels
  InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst_N.
Pfam; PF00538; linker histone; I.
Probos, PD000131; Linkerhist_N; 1.
Probos, P0000131; Linkerhist_N; 1.
SEQUENCE 232 A4; 24693 MW; 2D006AE44A8FA037 CRC64;
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   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUAR-2001 (TrEMBLrel. 16, Last annotation update)
Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
  DB 5;
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001395
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4

Indels 33; Gaps

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39.4%; Pred. No. 0.00045;
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RESULT 13

8 셤 ઠે 셤

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47 KKYAKEAAKAKKEAYKAEAKKYAKAAK ---AEKKEYAAAEAKKAEAAKAYKAEAAKAAA 102
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  MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
  SEQUENCE FROM N.A.
MEDLINE-20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
  SEQUENCE FROM N.A.
MEDLINE=96187795; PubMed=8614977;
Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.,
Lanalysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
posttions 88 to 182.";
Virology 216:102-123(1996).
   Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBL_TaxID=10506;
  SEQUENCE FROM N.A.
Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DRC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 142580; AAC96576.1; -.
IntorPro; IPRR002048; EF-hand.
PROSITE; PSO0018; EF HAND; UNKNOWN 1.
SEQUENCE, 311 AA; 35390 MW; 9780E9E9E2AFEF88A CRC64;
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
  SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
  to the EMBL/GenBank/DDBJ databases
  to the EMBL/GenBank/DDBJ databases
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   Virology 263:254-262(1999)
  PRELIMINARY;
  Virology 276:27-36(2000)
  Van Etten J.L.;
Submitted (MAY-1997)
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Submitted (DEC-1995)
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   103 KEAAYEA 109
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199 EAKAKEA 205
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        Action 2
        Action 3
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Search completed: March 10, 2003, 12:25:59 Job time : 58.7194 secs

4;

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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein

March 10, 2003, 12:15:01; Search time 56.7996 Seconds (without alignments) 255.712 Million cell updates/sec Run on:

US-09-816-989A-7 519 Title: Perfect score:

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Total number of hits satisfying chosen parameters:

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seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | Description          | Copolymer molecula | Copolymer molecula | Copolymer molecula | Copolymer molecula | Recombinant copoly | Recombinant copoly | Copolymer molecula | Peptide #10 used i | Amino acid polymer | Poly-Lys-Ala used |
|-----------|--------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| SUMMAKIES |        | ID                   | AAY82577           | AAY82576           | AAY82575           | AAY82574           | AAR06445           | AAR06446           | AAY82573           | AAY98499           | AAY59044           | AAU04289          |
|           |        | DB                   | 21                 | 21                 | 21                 | 21                 | 11                 | 11                 | 21                 | 21                 | 21                 | 22                |
|           |        | ce Match Length DB I | 109                | 98                 | 77                 | 99                 | 154                | 106                | 26                 | 100                | 100                | 100               |
|           | * 6    | Match                | 100.0              | 60.2               | 55.7               | 44.0               | 40.3               | 36.0               | 34.8               | 34.6               | 34.6               | 34.6              |
|           |        | Score                | 519                | 312.5              | 289                | 228.5              | 209                | 187                | 180.5              | 179.5              | 179.5              | 179.5             |
|           | +[ייסם | No.                  | -                  | 8                  | ٣                  | 4                  | 2                  | 9                  | 7                  | 80                 | 6                  | 10                |

| Nucleic acid trans<br>Amino acid sequenc<br>Trypanosoma cruzi<br>Histone H1 isoform<br>Human histone H1.5 |                                  |                                                          | Human histone H1 i<br>Human histone H1 i<br>Human histone H1 i<br>Drosophila melanog<br>Plasmodium yoelii<br>Synthetic helical<br>Drosophila melanog<br>Adhesive polypepti | Antibiotic potenti<br>(Lys) 434 protein s<br>M. tuberculosis hi<br>M. tuberculosis hi<br>Listeria monocytog<br>Peptide #8 used in<br>Amino acid polymer<br>Poly.L-Lysine used<br>Nucleic acid trans<br>Peptide #2951 enco |
|-----------------------------------------------------------------------------------------------------------|----------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AANS45852<br>AAX14928<br>AAR84568<br>AAX34068<br>AAX34060                                                 |                                  | . , , ,                                                  | AAW29476<br>AAY574033<br>AAY574033<br>AAB62173<br>AAB62173<br>AAB24128<br>AAB63276<br>ABB63276<br>AAW44829                                                                 |                                                                                                                                                                                                                           |
| 100 22<br>223 20<br>643 16<br>158 20                                                                      | 010 +++ ++ 01 00                 | 218 20<br>218 21<br>218 21<br>130 23<br>130 23<br>219 23 | 222 18<br>222 20<br>222 20<br>607 22<br>507 21<br>140 13<br>299 22<br>111 18                                                                                               |                                                                                                                                                                                                                           |
|                                                                                                           |                                  |                                                          | 29.4<br>29.4<br>29.4<br>28.9<br>28.6<br>7.7                                                                                                                                |                                                                                                                                                                                                                           |
| 179.5<br>178<br>162.5<br>160.5                                                                            | 160.5<br>159.5<br>159.5<br>158.5 | 158<br>158<br>157.5<br>154.5<br>154.5                    | 152.5<br>152.5<br>152.5<br>151<br>150<br>148.5<br>144                                                                                                                      | 4444 .4444 .                                                                                                                                                                                                              |
| 112211122                                                                                                 | 114<br>118<br>119<br>20<br>21    | 22<br>24<br>25<br>26<br>27                               | 2 2 3 3 3 3 4 3 8 8 8 8 9 8 9 8 9 9 9 9 9 9 9 9 9 9 9                                                                                                                      |                                                                                                                                                                                                                           |

### ALIGNMENTS

AAY82577 standard; peptide; 109 AA 28-JUL-2000 (first entry) AAY82577; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

glatitamer accate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antibyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer; molecular weight marker; TV-marker; immune disease; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

06-APR-2000.

WO200018794-A1.

99WO-US22402. 24-SEP-1999;

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple callerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune ophoritis, autoimmune thyroiditis, autoimmune veoretinits, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-ses, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to molecular weights markers
   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
  Claim 10; Page 14; 72pp; English
   molecular weight markers.
  WPI; 2000-317499/27.
                         Lis D;
                      Gad A,
```

109 AA; Sequence

ô Gaps 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKEA 60 1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 . 0 100.0%; Score 519; DB 21; Length 109; 100.0%; Pred. No. 1.4e-36; ive 0; Mismatches 0; Indels 0 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 Conservative Best Local Similarity Matches 109; Conserv Query Match ઠે g ઠે

RESULT 2

AAY82576 standard; peptide; 86 AA

AAY82576;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antidyroid; antiinflammatory antidiabetic; thyromimetic; hemostatic; antipsoriatic; dermatological; antidianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris, systemic lupus erythematosus. 

Unfidentified

WO200018794-A1

98US-0101693. 99WO-US22402. 24-SEP-1999; 25-SEP-1998; 06-APR-2000.

CO LTD. (YEDA ) YEDA RES & DEV CO L' (TEVA-) TEVA PHARM USA INC.

Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune cueceinnitis, crohn's disease, formic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.

86 AA; Sequence

27; Gaps 21; Length 86; 3; Indels 60.2%; Score 312.5; DB 72.1%; Pred. No. 2e-19; iive 1; Mismatches 80; Conservative Query Match Best Local Similarity Matches

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1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60

1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA------36 g

61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109 ઠે

RESULT 3

AAY82575 standard; peptide; 77 AA. AAY82575;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hamemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; AAY82575

ID AAYK

AC AAZK

XX AAZK

XX XX AAZK

XX XX COPC

KW Glar

KW Glar

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for all the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune proportias, autoimmune cophoritis, autoimmune thyroiditis, autoimmune proportias, purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, disparkin myxoedema, myasthenia gravis peomphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-set include host-versus-graft disease, graft-versus-set of the invention have defined molecular weights and physpetides of the invention have allowed the contact sensitivity mysperies which are analogous to glatinamer actate molecules, which makes them ideal for use as
inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
  Claim 10; Page 14; 72pp; English.
  (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
   99WO-US22402.
  98US-0101693.
  molecular weight markers
  WPI; 2000-317499/27.
   WO200018794-A1
  Gad A, Lis D;
  25-SEP-1998;
   Unidentified
   24-SEP-1999;
  06-APR-2000.
```

4. Gaps 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60 32; Score 289; DB 21; Length 77; Pred. No. 1.6e-17; 1; Mismatches 3; Indels 3 55.7%; Query Match
Best Local Similarity 67.0.
To 73; Conservative 77 AA; Sequence ઢ

1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA-------61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109

셤

셤 ઠ

37 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77 RESULT 4

AAY82574 standard; peptide; 66 AA AAY82574; AAY82574
ID AAY8
XX
AC AAY8

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillan-Barre's syndrome; psoriasis; hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid seguence SEQ ID NO:4. 28-JUL-2000 (first entry) 

Unidentified

WO200018794-A1.

06-APR-2000,

99WO-US22402. 24-SEP-1999; 98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English.

weight TV-marker polypeptides from the present invention. The present weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for alsaesse which may be treated tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohn's disease, foronic immune thyroiditis, autoimmune coupering purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-vype hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as

66 AA; Sequence

Gaps 43; 44.0%; Score 228.5; DB 21; Length 66; 56.9%; Pred. No. 1.6e-12; Indels 0; Mismatches 62; Conservative Local Similarity Query Match Matches

4,

1 AKKYAKKAEKAYAKKAKAKAKEAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60 -- 25 1 AKKYAKK-EKAYAKAKA------EAKAAKKA-----

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61 УКАЕАККҮАКААКАБККЕУАААБАККАБААКАҮКАЕААКАААКБААҮБА 109  4

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AAR06446 standard; protein; 106 AA.
   Disclosure, Fig 12, 25pp, English.
  90US-0473845.
89US-0312541.
  90EP-0301700,
   (first entry)
   Conservative
                        92 AYKAEAAKAAAKEA 105
  142 KYKKEAEK--AKEA 153
   immunological activity
   (REPL-) REPLIGEN CORP
   WPI; 1990-255848/34.
   certain amino acids.
  Similarity
  See also AAQ05664.
  106 AA;
  N-PSDB; AAQ06446.
  fusion protein.
  16-FEB-1990;
  07-FEB-1990;
  17-FEB-1989;
   03-JAN-1991
   22-AUG-1990.
   90;
   EP383620-A.
   Synthetic
  AAR06446;
  Seguence
  Query Match
   Cook KS;
   Local
   Best Loca
Matches
  AAR06446
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  6
  To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRLE B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. It the COP-1 polypeptide may be cleaved from the fusion protein. TCOP-1-7 contains oilgonucleotide duplexes incoding the following segments: YKK, BAE, KAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein.
   82 EYKKKARAABABESKKRABABESABYKKYKKKAKAKYKKKAKBABKARAABESKAKBABYK 141
  20; Indels 34; Gaps
  45 BAKKYAKEAAKA--KKEAYKAEAKKYAKAAKAEK-----KEYAAAEAKKAEAA--K 91
  KKYAKKAEKA-----YAKKAKAAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
   24 KKKAKEAEKAKKAKYKKYKKEAEAAKAAKAAAAAAAAYKKEAEA--AAEAEKAKYKKKKAKEA 91
   The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
   Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
   Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
   Length 154;
  Recombinant copolymer 1-77, myelin basic protein analogue.
26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
   Score 209; DB 11;
Pred. No. 1.6e-10;
  8; Mismatches
   AAR06445 standard; protein; 154 AA.
  Disclosure; Fig 11; 25pp; English.
   40.3%;
   90US-0473845.
89US-0312541.
   90EP-0301700.
   Query Match
Query Local Similarity 53.7%,
Best Local Similarity 53.7%,
Angress 72; Conservative
  (first entry)
  (REPL-) REPLIGEN CORP
   WPI; 1990-255848/34.
   multiple sclerosis;
   154 AA;
   See also AAQ05665
   N-PSDB; AAQ05664.
  17-FEB-1989;
   07-FEB-1990;
  03-JAN-1991
  22-AUG-1990
  EP383620-A.
  Synthetic.
   Sequence
   AAR06445;
  Cook KS;
  N
   AAR06445

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AAR0

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AAR0

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ABR0

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O3-J

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ABR0

DI

O3-J

  RESULT 5
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins a methionine residue occurs between the Protein A and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. Sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, KRA, PAB, AAA KEA, AAA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
  AKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
  The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
  1 AKAAEKAKAAK-KAYEAEKAKAKYEAK--KAEKAEKAEKAEKAEKAKAKAKAKAEK-----
   20; Indels 18;
   Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
  Length 106;
  Producing genes encoding random polymers of aminoacid(s) - i producing recombinant polypeptide(s) with biological and/or
Recombinant copolymer 1-19, myelin basic protein analogue.
  36.0%; Score 187; DB 11;
55.0%; Pred. No. 7.7e-09;
iive 11; Mismatches 20;
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56 AA;

Sequence

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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosupressive; antithyroid; antiinflammatory; antiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; chnoic immune thrombocytopenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
  Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
   Copolymer; molecular weight marker; TV-marker; immune disease;
65 AKKYAKAAKAEKKEYAAAEAKKAEAA----KAYKAEAAKAAAK-EAAYE 108
        pemphigus vulgaris; systemic lupus erythematosus.
  AAY82573 standard; peptide; 56 AA
  (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
   99WO-US22402
  98US-0101693.
   28-JUL-2000 (first entry)
  WO200018794-A1.
   Lis D;
  25-SEP-1998;
  24-SEP-1999;
   Unidentified
  06-APR-2000.
   AAY82573;
   3ad A,
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include archritic conditions, antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves upworetinitis, contact sensitivity disease, diabetes mellitus, Graves upvoretinitis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves include host-versus-sare's syndrome, Hashimoto's disease, indiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated disease which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physpetides of the invention have analogous to molecular weights and physpetides which are analogous to molecular and proper myspecial properties which are analogous to appropriet and properties. AAY82571 to AAY82577 represent specifically claimed copolymer molecular Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases Claim 10; Page 14; 72pp; English molecular weight markers.

```
The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding nucleic acid to a cell. The system comprises a nucleic acid binding nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
   3;
  System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
   Gaps
  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
  Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
   53;
   34.6%; Score 179.5; DB 21; Length 100;
   34.8%; Score 180.5; DB 21; Length 56; 45.9%; Pred. No. 1.4e-08;
   Smith LC;
   61 YKABAKKYAKAAKAEKKEYAAABAKKABAAKAYKABAAKAAAKBAAYBA 109
  -------YKAEAAKAAKEAYEA 56
                                       3; Indels
  1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKAEAK-----
   Peptide #10 used in nucleic acid transporter system.
   WOO SLC,
   3; Mismatches
  Disclosure; Column 125-128; 108pp; English
   Sottchalk S, Sparrow J, Cristiano RJ,
   AAY98499 standard; Peptide; 100 AA.
  (BAYU ) BAYLOR COLLEGE MEDICINE.
   92US-0855389.
93WO-US02725.
   93US-0167641.
   31-JUL-2000 (first entry)
   Conservative
  WPI; 2000-281993/24.
Query Match
Best Local Similarity
  100 AA;
   14-DEC-1993;
   20-MAR-1992;
19-MAR-1993;
  degradation.
                                       50;
   US6033884-A
  07-MAR-2000
   Synthetic.
  AAY98499;
  Sequence
   Query Match
   Matches
  40
   AAY98499
ID AAY9
   RESULT 8
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WPI; 2000-317499/27.

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3;

Indels

DB 21; Length 100;

Score 179.5; DB 2 Pred. No. 3.1e-08; 8; Mismatches

34.6%; 55.6%;

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10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKKEAYKAEAKKY 68
   69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   Conservative
   Local Similarity
               100 AA;
  Misc-difference 3
  BAYU ) BAYLOR
   05-JUN-1995;
  14-DEC-1993;
   19-MAR-1993;
  US6177554-B1
  23-OCT-2001
   55;
  23-JAN-2001
   Synthetic
  WOO SLC,
               Sequence
  AAU04289;
   Sequence
  Query Match
   Matches
  09
  RESULT 10
   AAU04289
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   The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognises and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is apable of moving or initiating movement through cytosis; (c) a nucleic capable of moving or initiating movement through a nuclear membrane; or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The Allows again within the NTS avoids the problem of endosomal/lysosomal
               ۳,
  3.100
/note= "Lys-Ala in positions 3 to 100 may be optionally
  Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
               Gaps
                                     KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
  cytosis;
   Nucleic acid transport system, NTS; cell surface receptor; cytosi.
nuclear membrane; lysis moiety; transgenic animal; human disease;
               ÷.
  Smith LC;
              33; Indels
   Sparrow J,
  AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   60 АКАКАКАКАКАКАКАКАКАКАКАКАКАКАКАКАК
  Pred. No. 3.1e-08;
  Amino acid polymer seq ID NO: 64 of US5994109,
              8; Mismatches
   Disclosure; Columns 123-124; 107pp; English.
  Gottchalk S,
  Location/Qualifiers
   AAYS9044 standard; peptide; 100
  (BAYU ) BAYLOR COLLEGE MEDICINE
  nucleic acid delivery; cancer
  93U$-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
55.6%;
   95US-0460890.
   (first entry)
               55; Conservative
  Cristiano RJ,
   WPI; 2000-038262/03
  Best Local Similarity
  Key
Misc-difference 3
  20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
  07-MAR-2000
   03-JUN-1995;
   14-DEC-1993;
  US5994109-A
   30-NOV-1999
  degradation
  Synthetic
   AAY59044;
   WOO SLC,
                                      10
  69
              Matches
  AAY59044
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3;
   The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, lysis agents, spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic
  Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
   animals
   Gaps
   /note= "Lys-Ala in positions 3-100 may be present or
   3;
  Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
   Length 100;
  nucleic acid into specific cells e.g. in gene therapy to dacid into hepatocytes, muscle cells or bone forming cells.
  Sparrow
   Score 179.5; DB 22; Length
Pred. No. 3.1e-08;
8; Mismatches 33; Indels
   Poly-Lys-Ala used in nucleic acid transporter system.
  Gottchalk S,
  Disclosure; Column 131; 111pp; English.
  Location/Qualifiers 3..100
AAU04289 standard; Peptide; 100 AA
  Cristiano RJ,
  absent"
  COLLEGE MEDICINE
   34.6%;
   92US-0855389.
93WO-US02725.
   95US-0462040
  93US-0167641
  (first entry)
  34.6
Best Local Similarity 55.6
Matches 55; Conservative
  Smith LC,
   WPI; 2001-365933/38
  100 AA;
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nucleic acid the nucleic acid transporter system can also be used in a method con the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, and polypeptides, such as hormones, usual antigens, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
   Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                      Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
  Nucleic acid transporter system peptide ligand SEQ ID NO 64.
   WOO SIC;
   Cristiano RJ, Smith LC,
  AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   Disclosure; Column 125-126; 105pp; English.
   AAB45852 standard; Protein; 100 AA
   COLLEGE MEDICINE
   93US-0167641.
92US-0855389.
93WO-US02725.
   95US-0460971
  (first entry)
   Gottchalk S, Sparrow J,
  WPI; 2001-049093/06
   bacterial antigen.
   100 AA;
   (BAYU ) BAYLOR
   Unidentified
   20-MAR-1992;
19-MAR-1993;
   05-JUN-1995;
  14-DEC-1993;
  21-MAR-2001
  US6150168-A.
  21-NOV-2000
   AAB45852;
   Sequence
 10
  69
   AAB45852
ID AAB4
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The invention provides heat-killed Mycobacterium vaccae, or recombinant

M. vaccae proteins. The M. vaccae proteins may be employed to activate

T cells and natural killer cells, to stimulate the production of

cytokines, to enhance the expression of co-stimulatory molecules on

dendritic cells and monocytes, and to enhance dendritic cell maturation

and function. The proteins can be expressed by standard recombinant

methodology. Pharmaceutical compositions comprising the proteins or

nucleic acid sequences encoding the proteins can be used for the

treatment, prevention, and detection of disorders including infectious

diseases, immune disorders and cancer. In particular, the compounds and

methods are used for treatment of diseases of the respiratory system,

such as mycobacterial infections, asthma, allergies, tuberculosis,

leprosy, sarcoidosis and lung cancers, and disorders of the skin such as

psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,

alopecia areata, and skin cancers such as basal carcinoma, squamous cell
   Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
  Gaps
  Score 178; DB 20; Length 223;
Pred. No. 9.5e-08;
6; Mismatches 34; Indels 10;
 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                  Amino acid sequence of M. vaccae antigen GV-45.
  Tan P, Visser ES,
   Enhancing immune response to an antigen
  (GENE-) GENESIS RES & DEV CORP LTD.
   ġ
  squamous cell carcinoma; melanoma.
   Claim 1; Page 239; 243pp; English.
   AAY14928 standard; protein; 223
  98US-0205426.
97US-0996624.
97US-0997080.
97US-0997362.
  Query Match
34.3%;
Best Local Similarity 54.5%;
Matches 60; Conservative 6
   98WO-NZ00189
   98US-0156181
  Prestidge RL, Skinner MA,
  25-OCT-1999 (first entry)
   carcinoma and melanoma
  Mycobacterium vaccae.
  WPI; 1999-430163/36.
   223 AA;
  N-PSDB; AAZ11393.
   WO9932634-A2
   23-DEC-1998;
   17-SEP-1998;
  04-DEC-1998;
  23-DEC-1997;
23-DEC-1997;
   01-JUL-1999,
   23-DEC-1997
   AAY14928;
 69
                                  9
   AAY14928
ID AAY1
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Gaps

3,

33; Indels

8; Mismatches

55; Conservative Similarity

Matches

8

Query Match Best Local

34.6%; Score 179.5; DB 22; Length 100; 55.6%; Pred. No. 3.1e-08;

10 KAYAK-KAKAAKEKKAYAKKEAKAYKAABAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68

1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56

```
AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi

The proteins are all fusion products with glutathione-S-transferase

(GST) and some contain a linker sequence. The TCR27 protein comprises

a 95 amino acid (aa) N-terminal region; 69 repeats of a highly

conserved 14 as sequence and a 68 as C-terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69

repeat units and also contains the amino and carboxy terminal
peptides of TCR27. The TCR27 polypeptides of the invention are useful

for the diagnosis of Chagas disease (American Trypanosomiasis), they

are capable of detecting anti-T.cruzi antibodies; or for blood

screening. The TCR27 protein has epitopes to which most T cruzi
infected individuals have antibodies. The TCR27 polypeptides will not

react with serum from patients with laishmaniasis, schistosomiasis,

correction.
                   1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
  New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a
immunoassay reagent for specific diagnosis of Chagas disease, also
related nucleic acid and transformed cells
   Location/Qualifiers
329..552
/label= repeat region
/note= "16 of 69 repeat units of 14 amino acids"
  TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
   Trypanosoma cruzi TCR27 polypeptide, Ag15.
  Disclosure, Page 40-41; 68pp; English.
  AAR84568 standard; Protein; 643 AA
  95WO-US03191
   94US-0216894
  (first entry)
  positives in diagnosis.
  KIRCHHOFF L V.
  Kirchhoff LV, Otsu K;
   WPI; 1995-344618/44.
   643 AA;
   Trypanosoma cruzi
   N-PSDB; AAT05332
   OTSU K.
  WO9525797-A1.
  20-MAR-1995;
   24-MAR-1994;
  09-MAY-1996
   28-SEP-1995
   AAR84568;
   Sequence
   (KIRC/) (OTSU/)
  Key
Region
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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a porin antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the pANCA-reactive fragment, or presence or absence of the complex; where the presence of the complex indicates that the subject has UC. The pANCA-reactive histone H1-like antigen are useful in the antigen, porin antigen and Bacteroides antigen are useful in the antigen, porin antigen and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence represents a human histone H1 isoform H1.5 pANCA-reactive fragment.
   5
  Ulcerative colitis; histone; H1-like antigen; porin antigen; human; Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis; perinuclear anti-neutrophil cytoplasmic antibody; isoform.
445 AABATKVABABEKOKAABATKVABABEKOKAABATKVABABEKOKAABATKVABBABKOKAABA 504
  51 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
   7; Gaps
   1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAA----EAKKKAKAEAKKYAKEAAK 55
   Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
   57 KK--EAYKAEAKKYAKAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
  505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
   Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).
  DB 20; Length 158;
   56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
  Query Match 30.9%; Score 160.5; DB 20; Length Best Local Similarity 46.8%; Pred. No. 1.9e-06; Matches 51; Conservative 7; Mismatches 44; Indels
   Example 4; Page 125-126; 134pp; English
  Ş
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  99WO-US05492.
   (first entry)
  (REGC ) UNIV CALIFORNIA.
   WPI; 1999-551215/46.
  Cohavy 0;
  158 AA;
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   W09945955-A1
  12-MAR-1999;
   12-MAR-1998;
   23-NOV-1999
  16-SEP-1999.
  Braun J,
  AAY34068;
   RESULT 14
AAY34068
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Gaps

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us-09-816-989a-7.open.rag

```
Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
  The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a portin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. Sequences AAYS7362-367 represent pANCA-reactive fragments, derived from human histone HI.S.
   Ulcerative colitis; inflammatory bowel disease; porin antigen; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; human; histone H1; isoform; NANUC-2.
   DB 21; Length 158;
  Human histone H1.5 pANCA-reactive fragment (residues 69-226).
  30.9%; Score 160.5; DB 2:
ilarity 46.8%; Pred. No. 1.9e-06;
Conservative 7; Mismatches 44
   Example 4; Columns 69-70; 49pp; English.
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  98US-0041889.
   96US-0057846.
97US-0837058.
   (first entry)
  (REGC ) UNIV CALIFORNIA
  Query Match
Best Local Similarity
Matches 51; Conserva
   WPI; 2000-255695/22.
   Braun J;
  158 AA;
   12-APR-1996;
   Homo sapiens
   11-APR-1997;
  13-JUN-2000
   US6033864-A.
  07-MAR-2000
   Cohavy 0,
  Sequence
  AAY57366;
RESULT 15
                AAY57366
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Search completed: March 10, 2003, 12:21:31 Job time : 57.7996 secs

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7;

44; Indels

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56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104 

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March 10, 2003, 12:26:10 ; Search time 32.4241 Seconds (without alignments) 141.764 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   188354 segs, 42170167 residues
  OM protein - protein search, using sw model
   Gapop 10.0 , Gapext 0.5
   US-09-816-989A-7
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Perfect score:
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   Searched:
  Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                   | Sequence 7, Appli | Sequence 6, Appli | 'n               | 4                | Sequence 3, Appli | 01,               | ď,                | Sequence 24, Appl | 95,               | Sequence 8, Appli | Sequence 23, Appl |                  | Sequence 5, Appli | Sequence 36182, A   | Sequence 2, Appli | Sequence 5197, Ap  | Sequence 48, Appl | Sequence 11216, A   | Sequence 13765, A   |
|-------------------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|---------------------|-------------------|--------------------|-------------------|---------------------|---------------------|
| ID                            | US-09-816-989A-7  | US-09-816-989A-6  | US-09-816-989A-5 | US-09-816-989A-4 | US-09-816-989A-3  | US-10-051-643-201 | US-09-820-843A-27 | US-09-820-843A-24 | US-09-820-843A-95 | US-09-820-843A-8  | US-09-820-843A-23 | US-09-124-280A-3 | US-10-184-832-5   | US-09-864-761-36182 | US-09-816-989A-2  | US-09-738-626-5197 | US-09-999-724-48  | US-09-815-242-11216 | US-09-815-242-13765 |
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| &<br>Query<br>Match Length DB | 109               | 86                | 77               | 99               | 26                | 223               | 356               | 309               | 369               | 372               | 352               | 434              | 452               | 617                 | 45                | 9                  | 218               | 829                 | 892                 |
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| Score                         | 519               | 312.5             | . 289            | 228.5            | 180.5             | 178               | 162               | 154.5             | 153.5             | 153.5             | 144               | 144              | 143.5             | 138.5               | 138               | 126                | 122.5             | 122.5               | 122.5               |
| Result<br>No.                 | -                 | 7                 | m                | 4                | 2                 | 9                 | 7                 | œ                 | σ,                | 10                | 11                | 12               | 13                | 14                  | 15                | 16                 | 17                | 18                  | 19                  |

| Sequence 7, Appli | Sequence 100, App | Sequence 5, Appli | Sequence 10314, A     | Seguence 90, Appl | Sequence 46, Appl | Seguence 1, Appli | Sequence 2, Appli | Sequence 559, App | Sequence 1164, Ap  | Sequence 9, Appli | Sequence 38, Appl | Sequence 160, App   | Sequence 1, Appli | Sequence 7, Appli | Sequence 37061, A     | Sequence 268, App  | Sequence 5854, Ap  | Sequence 5, Appli | Sequence 1271, Ap  | Sequence 988, App | Seguence 988, App | Sequence 3538, Ap  | Sequence 39625, A   | Sequence 245, App  | Sequence 245, App |
|-------------------|-------------------|-------------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-----------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|---------------------|--------------------|-------------------|
| US-10-093-892-7   | US-09-919-497-100 | US-10-093-892-5   | ) US-09-815-242-10314 | US-09-999-724-90  | US-09-999-724-46  | US-09-882-774-1   | US-09-923-304-2   | US-09-925-302-559 | US-09-925-300-1164 | US-10-093-892-9   | US-09-765-272-38  | ) US-09-765-272-160 | US-09-816-989A-1  | US-09-820-843A-7  | ) US-09-864-761-37061 | US-09-881-752A-268 | US-09-738-626-5854 | US-09-820-843A-5  | US-09-925-301-1271 | US-09-925-299-988 | US-09-925-299-988 | US-09-738-626-3538 | US-09-864-761-39625 | US-09-978-295A-245 | US-09-978-697-245 |
| σ                 | 10                | σ                 | 10                    | σ                 | σ                 | σ                 | 10                | 10                | 10                 | σ                 | 10                | 10                  | 7                 | σ                 | 10                    | 10                 | 0                  | σ                 | 10                 | σ                 | 5                 | σ                  | 10                  | σ                  | 6                 |
| 96                | 582               | 105               | 890                   | 102               | 118               | 619               | 220               | 265               | 300                | 96                | 453               | 641                 | . 35              | 203               | 71                    | 452                | 365                | 172               | 363                | 606               | 606               | 272                | 87                  | 472                | 472               |
| 22.9              | 22.9              | 22.7              | 22.5                  | 22.2              | 22.2              | 22.2              | 21.7              | 21.7              | 21.5               | 21.2              | 20.4              | 20.4                | 20.5              | 20.1              | 20.0                  | 19.8               | 19.6               | 19.4              | 19.4               | 19.4              | 19.4              | 19.3               | 19.2                | 19.2               | 19.2              |
| 119               | 119               | 118               | 117                   | 115               | 115               | 115               | 112.5             | 112.5             | 111.5              | 110               | 106               | 106                 | 105               | 104.5             | 104                   | 103                | 101.5              | 100.5             | 100.5              | 100.5             | 100.5             | 100                | 99.5                | 99.5               | 99.5              |
| 20                | 21                | 22                | 23                    | 24                | 25                | 56                | 27                | 28                | 53                 | 30                | 31                | 32                  | 33                | 34                | 32                    | 36                 | 37                 | 38                | 39                 | 40                | 41                | 42                 | 43                  | 44                 | 45                |
|                   |                   |                   |                       |                   |                   |                   |                   |                   |                    |                   |                   |                     |                   |                   |                       |                    |                    |                   |                    |                   |                   |                    |                     |                    |                   |

## ALIGNMENTS

JS-09-816-989A-7

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: ADD FOR THERALEUTIC USE
FITLE OF INVENTION: ADD FOR THERALEUTIC USE
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CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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   US-09-816-989A-7
  LENGTH: 109
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YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 RESULT 2 US-09-816-989A-6 ; Sequence 6, Application US/09816989A g ò

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| Sequence 4, Application US/09816989A
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| APPLICANT: Lis, Doris
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| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| FILE REFERENCE: 2609/60807-A-PCT-US
| CURRENT FILING DATE: 2001-03-23
| PRIOR APPLICATION NUMBER: 60/101,693
| PRIOR PILING DATE: 1999-09-25
| PRIOR APPLICATION NUMBER: POT/US99/22402
| PRIOR PILING DATE: 1999-09-24
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| SEQ ID NO 4
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
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US-09-816-989A-4
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62; Conservative 0; Mismatches 4
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Best Local Similarity
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Best Local Similarity
Matches 62; Conserva
   RESULT 4
US-09-816-989A-4
  RESULT 5
US-09-816-989A-3
  Matches
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APPLICANT: Lis, Doris
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
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PRIOR FILING DATE: 1998-09-24
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 05/99/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHIN VERSION 3.1
SEQ ID NO S: 7
LENGTH: 77
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2
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   FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
  Gaps
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   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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  27;
  3; Indels 32;
   DB 10; Length 86;
   Length 77;
   6 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
  1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA------1
  37 -KYEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77
  Indels
  60.2%; Score 312.5; DB 10; 72.1%; Pred. No. 1.5e-18; tive 1; Mismatches 3;
   1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA---
   Query Match 55.7%; Score 289; DB 10; Best Local Similarity 67.0%; Pred. No. 9.1e-17; Matches 73; Conservative 1; Mismatches 3;
   Sequence 5, Application US/09816989A Patent No. US20020115103A1
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ORGANISM: Artificial Sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
  Conservative
US20020115103A1
   Query Match
Best Local Similarity
  RESULT 3
US-09-816-989A-5
   80;
   FEATURE:
   Best Loca
Matches
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Sequence 24, Application US/09820843A
Publication No. US20030039963A1
Publication No. US20030039963A1
Publication No. US20030039963A1
APPLICAMT: COUNCIL Of Scientific and Industrial Research
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
  RESULT 9

US-09-820-843A-95

US-09-820-843A-95

Sequence 95, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES

CURRENT PAPLICATION UNUMBER: US/09/820,843A

CURRENT PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.0

SEQ ID NO 95

LENGTH: 369
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                                     57 KKEAYKAEAKKYAK-----AAKAEK----KEYAAAEAKKAEAAKAYKAEAAKA 100
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  3 KYAKKAEKAYAKK--AKAAKEKKAYAKKEAKAYKAAEAKKK----AKAEAKKYAKEAAKA 56
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  7;
   55 K-AKKBAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   NAME/KEY: misc_feature
) OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF
) NAME/KEY: misc_feature
) OTHER INFORMATION: gi|9951352
US-09-820-843A-24
  Length 309;
  Indels
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CTHER INFORMATION: conserved hypothetical protein;
NAME/KEY: misc_feature
NAME/REY: misc_feature
US-09-820-843A-95
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ORGANISM: Pseudomonas aeruginosa
   TYPE: PRT
ORGANISM: T. pallidum
  101 AAKEAAYEA 109
  230 EAERKAQEA 238
  US-09-820-843A-24
  SEQ ID NO 24
LENGTH: 309
  요
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  셤
   Sequence 27, Application US/09820843A

Sequence 27, Application US/09820843A

Sequence 27, Application US/09820843A

Publication No. 1220030039963A1

GENERAL INFORMATION: A COMPUTATION A METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI

TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES

FILE REFERENCE: Q63915

CURRENT APPLICATION MUMBER: US/09/820,843A

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SSGTWARE: PatentIn version 3.0

SSGTWARE: PatentIn version 3.0
   Sequence 201, Application US/10051643

| Sequence 201, Application US/10051643
| Publication No. US20020197265A1
| GENERAL INFORMATION: Of The Compounds for the Treatment APPLICANT: WASON, James D. | APPLICANT: WASON, James D. | TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory TITLE OF INVENTION: System using Mycobacterium Vaccae FILE REFERENCE: 11000.1008c2 | CURRENT PAPLICATION NUMBER: US/10/051,643 |
| PRIOR PAPLICATION NUMBER: US/09/156,181 |
| PRIOR PILING DATE: 1998-09-17 |
| PRIOR FILING DATE: 1998-09-17 |
| PRIOR FILING DATE: 1997-12-23 |
| NUMBER OF SEQ ID NOS: 208 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 201 |
| LEMCTH: 223 |
| LEMCTH: 223 |
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  112 АККААККАРАККАРАККАРРАККАРАККА-АТКААРАККАТААККААРАККАТРАККАДР
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Pred. No. 1.3e-07;
6; Mismatches 34; Indels 10; Gaps
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  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
  Length 356;
  61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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31.2%; Score 162; DB 9; Length 356
Best Local Similarity 42.6%; Pred. No. 3.6e-06;
Matches 55; Conservative 13; Mismatches 37; Indels
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CTHER INFORMATION: tolA protein
NAME/KEY: misc feature
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US-09-820-843A-27
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; ORGANISM: Mycobacterium vaccae
US-10-051-643-201
  Query Match
Best Local Similarity 54.5%;
Matches 60; Conservative
  ORGANISM: Vibrio cholerae
  RESULT 6
US-10-051-643-201
  TYPE: PRT
```

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APPLICANT: POITO, MASSIMO
TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
TITLE OF INVENTION: NEGATIVE BACTERIAL INFECTIONS AND ENDOTOXIN RELATED DISEASES
CORRESPONDENCE ADDRESS: 45
  ж
;
   ö
  56 -----AKKEAYKAEAKKYAK-----AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
   224 PAAKTAAAKPAAKPAAKPVAKPTAKPAAKTAAAKPAAKPAAKPAAKPAAKPAAKPVAKSAAAKP 283
   164 акраакраакраақтааакраакртакраакраакраақтааакраакраакруакраак 223
   1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAK----AYKAAEAKKKAKAEAKKYAKEAAK 55
  2 KKYAKKAEKAYAKKAKAKAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY 61
  ;
0
  Length 434;
  Length 352;
  53; Indels
   Indels
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PS/2
  62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKE 104
   Query Match 27.7%; Score 144; DB 10; Best Local Similarity 36.9%; Pred. No. 0.00011; Matches 38; Conservative 14; Mismatches 51;
                                     Score 144; DB 9;
Pred. No. 9.2e-05;
                         E: Hedman, Gibson & Costigan
1185 Avenue of the Americas
   COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,280A
FILING DATE: July 29,1998
   Sequence 3, Application US/09124280A Patent No. US20020034520A1
  NAME: COSTIGAN, James V.
REGISTRATION NUMBER: 25,669
REFREENCE/DOCKET NUMBER: 576-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989
INFORMATION FOR SEQ ID NO: 3:
   ATTORNEY/AGENT INFORMATION:
  : 434 amino acids
amino acid
                                 Query Match
Best Local Similarity 44.0
Matches 55, Conservative
  SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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   GENERAL INFORMATION:
   CITY: New York
STATE: New York
   USA
  105 AAYEA 109
  284 AAKPA 288
  10036
   ADDRESSEE:
STREET: 11
US-09-820-843A-23
   TOPOLOGY:
  US-09-124-280A-3
  US-09-124-280A-3
   COUNTRY:
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  APPLICANT: Counties:
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USFFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USFFUL AS ANTI-INFECTIVES
TILE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SEQ ID NO S: 2001-03-30
SEQ ID NO S: 2001-03-30
LENGTH: 372
  US-09-843A-23
Sequence 23, Application US/09820843A
Sequence 23, Application US/09820843A
Sequence 23, Application US/09820841
Sequence 23, Application US/0303039963A1
GENERAL INFORMATION:
THIS OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILLE REFERENCE: 63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent In version 3.0
   4
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  Gaps
   6 KKAEKAYAKKAKAAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKA-KKEAYKAE 64
  6 KKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA-YKAE 64
  .
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                     Length 369;
  Length 372;
  NAME/KEY: misc_feature
CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc_feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
  289 RKEAEEARRKEAEEARRKEAEEARRKEAEEARRKEAEFEA 336
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  65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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OTHER INFORMATION: alginate regulatory protein AlgP
NAME/KEY: misc feature
OTHER INFORMATION: g1|9951563
                     DB 9;
   30;
  DB 9;
                  29.6%; Score 153.5; DB 9, ilarity 39.8%; Pred. No. 1.7e-05; Conservative 26; Mismatches 30,
  Score 153.5; DB 9
Pred. No. 1.8e-05;
  20; Mismatches
   Sequence 8, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
  ORGANISM: Pseudomonas aeruginosa
  29.6%;
  Query Match 29.08
Best Local Similarity 45.38
Matches 48; Conservative
  ORGANISM: H. influenzae
              Query Match
Best Local Similarity
Matches 43; Conserve
  RESULT 10
US-09-820-843A-8
   SEQ ID NO 23
LENGTH: 352
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  196
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Sequence 2. Application US/09816989A
; Sequence 2. Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
    APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; SOFTWARE PETENT OF THE POST OF THE
   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
  5 AKKAEKAYAK---KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAK---- 57
   36; Indels 37;
  DB 10; Length 617;
   INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
INFORMATION: EXPRESSED IN HELAO, SIGNAL = 0.94
INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.3
INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
INFORMATION: SWISSPROT HIT: P12036, EVALUE 2.00e-33
INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
FRICK FILING DATE: 2001-01-00

FRICK APPLICATION NUMBER: PCT/US01/00661

FRICK APPLICATION NUMBER: PCT/US01/00601

FRICK PILING DATE: 2001-01-30

FRICK FILING DATE: 2001-01-30

FRICK APPLICATION NUMBER: US 60/234,687

FRICK APPLICATION NUMBER: US 60/234,687

FRICK APPLICATION NUMBER: US 69/608,408

FRICK PILING DATE: 2000-06-30

FRICK PILING DATE: 2000-06-30

FRICK PILING DATE: 2001-01-29

NUMBER: OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 36182

LENGRH: 617
  Query Match 26.7%; Score 138.5; DB 10
Best Local Similarity 35.3%; Pred. No. 0.00044;
Matches 49; Conservative 17; Mismatches 36
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   93 YKAEA-----AKAAAKEAA 106
   TYPE: PRT
ORGANISM: Homo sapiens
   OTHER INFORMATION:
  US-09-864-761-36182
   RESULT 15
US-09-816-989A-2
  FEATURE:
  OTHER
OTHER
OTHER
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   PREMERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Cann, Wensheng
TITLE OF INVENTION: EURE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERRACE: A001-02-23
FRIOR PELICATION NUMBER: US 60/120, 456
FRIOR PELICATION NUMBER: US 60/207, 456
FRIOR PELICATION NUMBER: PCT/US01/00666
FRIOR PELICATION NUMBER: PCT/US01/00667
FRIOR PELICATION NUMBER: PCT/US01/00667
FRIOR PELICATION NUMBER: PCT/US01/00669
   Sequence 5, Application US/10184832
Publication No. US20030022857A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu et al.
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REFERENCE: MPI2001-056F1NM
CURRENT APPLICATION NUMBER: US/10/184,832
CURRENT FILING DATE: 2002-06-28
PRIOR FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASTSEQ for Windows Version 4.0
  94 aeaeakaepkaeaeaepkaeaepkaeaeneaeakaeakaea-kaeakaeakaea-ka
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; Pred. No. 0.00013;
11; Mismatches 33;
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Patent No. US20020048763A1
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  46; Conservative
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ORGANISM: Mus musculus
US-10-184-832-5
  Query Match
Best Local Similarity
Matches 46; Conserva
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  10-184-832-5
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Gaps

4; Gaps Query Match 26.6%; Score 138; DB 10; Length 45; Best Local Similarity 76.6%; Pred. No. 3.4e-05; Matches 36; Conservative 0; Mismatches 7; Indels

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Search completed: March 10, 2003, 12:53:45 Job time : 33.5669 secs

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  Sequence 64, Appl
   March 10, 2003, 12:15:04 ; Search time 19.3165 Seconds (without alignments) 166.029 Million cell updates/sec
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  Description
   Sequence 3
Sequence 3
Sequence 3
  Sequence
Sequence
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| /cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd
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US-08-462-040-64
US-09-205-426-201
US-09-205-426-201
US-09-205-426-201
US-09-2015-746-8
US-09-041-889-32
US-09-041-889-32
US-09-041-889-4
US-08-929-329-5
   US-08-460-890A-62
US-08-167-641C-62
US-08-460-971A-62
US-08-462-040-62
US-09-041-889-1
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   Post-processing: Minimum Match 0%
Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
  US-09-816-989A-7
519
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Match Length
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   Perfect score:
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179.5
179.5
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162.5
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158.5
158.5
158.5
158.5
158.5
158.5
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Maximum DB
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  Searched:
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   Result
No.
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| Sequence 8, Appli | US-08-762-106-8   | N  | 516  | 23.8 | 123.5 | 45 |
| 23,               | US-08-894-017-23  | m  | 1561 | 24.0 | 124.5 | 44 |
| Sequence 6, Appli | US-08-993-008A-6  | 4  | 26   | 24.4 | 126.5 | 43 |
| Sequence 51, Appl | US-09-256-976-51  | 4  | 263  | 24.7 | 128   | 42 |
| Sequence 51, Appl | US-08-993-674A-51 | 4  | 263  | 24.7 | 128   | 41 |
|                   | US-08-834-306-51  | 3  | 263  | 24.7 | 128   | 40 |
|                   | US-08-557-309B-51 | N  | 263  | 24.7 | 128   | 39 |
| Sequence 1, Appli | US-08-929-414-1   | ~  | 262  | 24.7 | 128   | 38 |
| Sequence 1, Appli | US-08-403-379A-1  | -1 | 262  | 24.7 | 128   | 37 |
| Sequence 2, Appli | US-08-837-058-2   | c  | 220  | 25.0 | 129.5 | 36 |
| Sequence 2, Appli | US-09-041-889-2   | m  | 220  | 25.0 | 129.5 | 32 |
| Sequence 13, Appl | US-08-837-058-13  | m  | 147  | 25.0 | 129.5 | 34 |
| Sequence 13, Appl | US-09-041-889-13  | ٣  | 147  | 25.0 | 129.5 | 33 |
| Sequence 14, Appl | US-08-837-058-14  | m  | 113  | 25.0 | 129.5 | 32 |
| Sequence 14, Appl | US-09-041-889-14  | m  | 113  | 25.0 | 129.5 | 31 |
| Sequence 2, Appli | US-08-293-284A-2  | ~  | 433  | 25.6 | 133   | 30 |
| Sequence 2, Appli | US-08-346-849-2   | н  | 433  | 25.6 | 133   | 29 |
| Sequence 1, Appli | US-08-837-058-1   | ო  | 212  | 25.7 | 133.5 | 28 |

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| Sequence 64, Application US/08460890A |
| Sequence 64, Application US/08460890A |
| Patent No. 5994109 |
| GENERAL INFORMATION |
| APPLICANT: Word, Savio L.C. |
| APPLICANT: Cristiano, Richard J. Stephen |
| TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE |
| NUMBERS OF SEQUENCES: 65 |
| CONTRESPONDENCE ADDRESS: ADDRESSES: 1, ADDRES
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10 КАҮАК-КАКААКЕККАҮАККЕАКАУКААБАКККАКАБАККҮАКБААКАККЕАУКАБАККУ 68
  ٠.
۳
                                 Length 100;
  ; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be in OTHER INFORMATION: present or absent.

US-08-460-971A-64
   34.6%; Score 179.5; DB 4; Length 100;
  Indels
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Pred. No. 7.5e-09;
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  8; Mismatches
  Sequence 64, Application US/08460971A
Patent No. 6150168
  32,327
  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
                                   Query Match
Best Local Similarity 55.6%;
Matches 55; Conservative
  NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
   single
linear
   TOPOLOGY: "linear
MOLECULE TYPE: peptide
   STRANDEDNESS:
 US-08-167-641C-64
   US-08-460-971A-64
   Query Match
  원
  ઠે
   'n,
  10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
  Sequence 64, Application US/08167641C
Fatent No. 6033884
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
  Query Match
34.6%; Score 179.5; DB 2; Length 100;
Best Local Similarity 55.6%; Pred. No. 7.5e-09;
Matches 55; Conservative 8; Mismatches 33; Indels 3
   OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-890A-64
   OTHER PAPERMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
   69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   MEDIUM TYPE: storage
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION MUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION MUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/1993/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg' Richard J.
REGISTRATION NUMBER: 205/012
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg' Richard J.
REGISTRATION NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 205/012
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
   ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
  STREET: Lyon & Lyon STREET: STREET: Suite 4700 CITY: Los Angeles STATE: California CONTRY: U.S A
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
  US-08-167-641C-64
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   ò
  셤
```

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10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UM-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 31-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 11000.10
REFERENCE/DOCKET NUMBER: 11000.10
TELECOMMUNICATION INFORMATION:
  Sequence 201, Application US/09095855; Patent No. 6160093; GENERAL INFORMATION:
   TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
  LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
   SEQUENCE CHARACTERISTICS
  INFORMATION FOR SEQ ID NO:
  , MOLECULE TYPE: protein US-09-095-855-201
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
   linear
   CITY: Seattle
   USA
   ZIP: 98121
  US-09-095-855-201
   COUNTRY:
   69
   RESULT 5
   g
   셤
   à
  8
  ä
  Gaps
                                    3; Gaps
   10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
  3;
   APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchark, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
  Length 100;
  OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-462-040-64
                                 33; Indels
  Indels
  DB 4;
  Query Match 34.6%; Score 179.5; DB 4; Best Local Similarity 55.6%; Pred. No. 7.5e-09; Matches 55; Conservative 8; Mismatches 33;
   69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
  Best Local Similarity 55.6%; Pred. No. 7.5e-09;
Matches 55; Conservative 8; Mismatches 33
   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5. Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: IBM Compatible OPERATING SYSTEM: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 APPLICATION NUMBER: US/08/462,040 FILING DATE: June 5, 1995
CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/165,389 FILING DATE: March 19, 1993 APPLICATION NUMBER: PCT/US93/02725 FILING DATE: March 20, 1992 APPLICATION NUMBER: PCT/US93/02725 FILING DATE: March 19, 1993 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 212/078 TELEPONMUNICATION INPORMATION: TELEPONMUNICATION INPORMA
   Sequence 64, Application US/08462040 Patent No. 6177554 GENERAL INFORMATION:
  LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  RY: U.S.A.
90071-2066
   US-08-462-040-64
  RESULT 4
  셤
   ઠે
```

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ŝ
  APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
  112 ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
34; Indels 10; Gaps
   1 AKKYAKK--AEKAYAKKAKAKAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
  Query Match 34.3%; Score 178; DB 4; Length 223; Best Local Similarity 54.5%; Pred. No. 2.2e-08; Matches 60; Conservative 6; Mismatches 34; Indels
  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
  AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
   60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKA 98
   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
  11000.1002c3
```

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904136
  FILING DATE:
  US-09-115-746-8
TELEX:
   셤
   ò
   g
  à
   5
  Gaps
  1 AKKYAKK--AEKAYAKKAKAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
   10;
  Sequence 8, Application US/08216894
| Patent No. 5876734
| GENERAL INFORMATION:
| APPLICANT: Kirchhoff, Louis V. APPLICANT: Otsu, Keiko
| TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
| NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
| CITY: Washington, D.C.
  Sequence 201, Application US/09205426

Patent No. 6406704

GRUERAL INFORMATION:
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.100.204
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT APPLICATION NUMBER: 09/095,855
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER PILING DATE: 1997-06-12
EARLIER PILING DATE: 1997-06-12
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29
SOFTWARRE: FILING DATE: 1996-08-29
SOFTWARRE: PASEC for Windows Version 3.0
SEQ ID NO 201
ENGITH: 223
   34.3%; Score 178; DB 4; Length 223; 54.5%; Pred. No. 2.2e-08; Live 6; Mismatches 34; Indels
  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATORNEY AGENT IRFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
   ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-201
  (202) 672-5300
(202) 672-5399
   Best Local Similarity 54.5
Matches 60; Conservative
   RY: USA
20007-5109
  TELEPHĜNE:
                   RESULT 6
US-09-205-426-201
  COUNTRY:
  US-08-216-894-8
  TELEFAX:
  Query Match
   g
  ઠ
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4
  11; Gaps
  1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56
   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56
  57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
   505 TKVAEAEKQKAAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
  Sequence 8, Application US/09115746

Patent No. 6228601

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Cteu, Keiko

TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES:

ADDRESSEE: Foley & Lardher

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA
  Length 643;
  DB 4; Length 643;
  Indels
  Indels
   COMPARTIES READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: A PACENTIN Release #1.0, Version #1.25
SOFTWARE: PACENTIN BATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR PALCATION DATA:
APPLICATION NUMBER: 08/216,894
  31.3%; Score 162.5; DB 2; ilarity 44.4%; Pred. No. 1.3e-06; Conservative 18; Mismatches 36;
   31.3%; Score 162.5; DB 4; ilarity 44.4%; Pred. No. 1.3e-06; Conservative 18; Mismatches 36;
   85326/102/DRLO
   ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 8532
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
inPormation For SEQ ID NO: 8:
SEQUENCE CHRACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECTLE TYPE: Dinear
MOLECTLE TYPE: Protein
US-08-216-894-8
  TELBEAX: (202,
TELBEAX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acids
TYPE: Tinear
  ; MOLECULE TYPE: protein US-09-115-746-8
  Query Match
Best Local Similarity
Matches 52; Conserva
   Query Match
Best Local Similarity
Matches 52, Conserv?
```

```
NUMBER OF SEQUENCES:
  amino acid
   Query Match
Best Local Similarity
  FILING DATE:
  US-09-041-889-32
   TOPOLOGY:
   LENGTH:
   Matches
   ઠે
   g
  ð
   APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
   Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC pANCA antigens
   'n
   51 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
   Gaps
   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAA-----EAKKKAKAEAKKYAKEAAK 55
57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
                            505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
  DB 3; Length 158;
  56 AKKBAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
  109 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKPKAAKK 157
   44; Indels
   ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/041,889
FILING DATE:
  30.9%; Score 160.5; DB 3
46.8%; Pred. No. 4.6e-07;
tive 7; Mismatches 44
   FILING DAIE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
   Sequence 32, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Previ
   Sequence 40, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
   Best Local Similarity 46.8
Matches 51, Conservative
  / MOLECULE TYPE: peptide
US-09-041-889-40
  US-09-041-889-40
   US-09-041-889-32
  Query Match
   RESULT 10
  δ
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  d
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119 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 176
  Gaps
  1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAA-----EAKKKAKAKAEAKKYAKEAAK 55
   7;
  30.9%; Score 160.5; DB 3; Length 226; 46.8%; Pred. No. 6.6e-07; tive 7; Mismatches 44; Indels 7
   177 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKKAAAKK 225
  DIAGNOSING INFECTION
   56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR.1994
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
  us-08-216-894-10
; Sequence 10, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAG;
; TITLE OF INVENTION: WITH TRYPANOSOMA CRUZ.
; ANDRESSEE: Foley & Larchner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READANITE
  POLYPEPTIDES FOR DIAGN WITH TRYPANOSOMA CRUZI
   NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
   PC-DOS/MS-DOS
  COUNTRA.
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
PETINGER: IBM PC COMPATIBLE
PC-DOS/MS.
   FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
   226 amino acids
   51; Conservative
  MOLECULE TYPE: peptide
  COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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RESULT 14
   셤
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  Gaps
   1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56
   57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEA 105
   375 TKVAEABKQKAABEATKVAEABKQKAABATKVAEABKKQKAABATKVABABEKQKAABA 430
  US-09-115-746-10

Sequence 10, Application US/09115746

Fatent No. 6228601

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Octsu, Keiko

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

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STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner

STREET: ADDRESSEE: Foley & Lardner
   Length 472;
  Score 158.5; DB 4; Length 472; Pred. No. 2e-06;
   30.5%; Score 158.5; DB 2; Length 44.0%; Pred. No. 2e-06; Live 18; Mismatches 36; Indels
  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 85326/102/DRLO

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
CENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MALECULE TYPE: protein
US-08-216-894-10
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET WINDRER: 85326/102/DRLO
TELECHMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
   TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
  30.5%;
  : 472 amino acids
amino acid
   Best Local Similarity 44.0 Matches 51; Conservative
   ; MOLECULE TYPE: protein US-09-115-746-10
  Query Match?
Best Local Similarity
   linear
  FILING DATE:
  TOPOLOGY:
  LENGTH:
   Query Match
   RESULT 12
   셤
   ઠે
```

```
4.
  4
   315 AAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEA 374
   11; Gaps
  1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYA----KEAAKA 56
  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKKAKAEAKKYA----KEAAKA 56
  375 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 430
  57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEA 105
  57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAKKA 105
  491 TKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEA 546
  DB 2; Length 564;
   APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
  Sequence 2, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: CRITCHOOFF, Louis V.
APPLICANT: OF SECOND CRITCHOOFF, TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INPECTION
; TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
Matches 51; Conservative 18; Mismatches 36; Indels
   Indels
   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERRATION NUMBER: 85326/102/DRLO
TELECOMMUNICATION: INFORMATION:
   30.5%; Score 158.5; DB 2;
44.0%; Pred. No. 2.4e-06;
tive 18; Mismatches 36;
   US-08-216-894-2
; Sequence 2, Application US/08216894
; Patent No. 5876734
   ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
   TELEX: 904136
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 564 amino acids TYPE: amino acid TOPOLOGY: linear
  (202) 672-5300
  TELEPHONE: (202) 0, 2099
   51; Conservative
  MOLECULE TYPE: protein US-08-216-894-2
  Best Local Similarity
Matches 51; Conserva
  GENERAL INFORMATION:
   US-09-115-746-2
   Query Match
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NUMBER OF SEQUENCES: 10

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Search completed: March 10, 2003, 12:30:04 Job time : 20.3165 secs
  : 218 amino acids
amino acid
  LOCATION: 1.218
OTHER INFORMATION:
   NAME/KEY: Peptide
   TYPE: amir
TOPOLOGY:
  US-09-041-889-4
  셤
  ð
  GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Charay, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
  11; Gaps
   1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYA----KEAAKA 56
  57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAKEA 105
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ZIF: 20007-5109
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
  ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
  APPLICATION:
PILING DATE:
ATTORNEY/BENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
  Sequence 4, Application US/09041889 Patent No. 6033864
   : 564 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
US-09-115-746-2
  CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
   US-09-041-889-4
   LENGTH:
   윰
  ઠે
   Š
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108 KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAA--G 165
   2 KKYAKKAEKAYAKKAKAKEKK--AYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
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H1-S-4"
              PRICE APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058
FILING DATE: 11.APR.1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 anino acids
CLASSIFICATION
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